

SPLICE FORM 1 (cdna sequence):

```
1 GTGAGTCATA TGAAAGCTCC ACGCTGCTGA CCTCTGGCAA AAAGGGAGAG
51 AACAAAGGATA GGAGAGGCAG TGGGGGAAAAG GTTCAAGTGC GGGTTTTTCTC
101 CTTGAACCTA GAAGATTATG GGTCAAGAGC TGTGTGCAAA GACTGTACAG
151 CCTGGATGCA GCTGCTACCA TTGTTTCAGAG GGAGGCGAGG CACACAGCTG
201 TCGGAGGAGT CAGCCTGAGA CCACGGAGGC TGC GTTCAAG CTAACAGACC
251 TAAAAGAAGC ATCATGTTCC ATGACTTCAT TTCACCCCAG GGGACTTCAA
301 GCTGCCCCGTG CCCAGAAGTT CAAGAGTAAA AGGCCACGGA GTAACAGTGA
351 TTGTTTTTCAG GAAGAGGATC TGAGGCAGGG TTTTCAGTGG AGGAAGAGCC
401 TCCCTTTTGG GGCAGCCTCA TCTTACTTGA ACTTGGAGAA GCTGGGTGAA
451 GGCTCTTATG CGACAGTTTA CAAGGGGATT AGCAGAATAA ATGGACAAC T
501 AGTGGCTTTA AAAGTCATCA GCATGAATGC AGAGGAAGGA GTCCCATTTA
551 CAGCTATCCG AGAAGCTTCT CTCCTGAAGG GTTTGAAACA TGCCAATATT
601 GTGCTCCTGC ATGACATAAT CCACACCAAA GAGACACTGA CATTCTGTTT
651 TGAATACATG CACACAGACC TGGCCAGTA TATGTCTCAG CATCCAGGAG
701 GGCTTCATCC TCATAATGTC AGACTTTTCA TGTTTCAACT TTTGCGGGGC
751 CTGGCGTACA TCCACCACCA ACACGTTCTT CACAGGGACC TGAAACCTCA
801 GAACTTACTC ATCAGTCACC TGGGAGAGCT CAAACTGGCT GATTTTGGTC
851 TTGCCCAGGC CAAGTCCATT CCCAGCCAGA CATACTCTTC AGAAGTCGTG
901 ACCCTCTGGT ACCGGCCCCC TGATGCTTTG CTGGGAGCCA CTGAATATTC
951 CTCTGAGCTG GACATATGGG GTGCAGGCTG CATCTTTATT GAAATGTTCC
1001 AGGGTCAACC TTTGTTTCCT GGGGTTTCCA ACATCCTTGA ACAGCTGGAG
1051 AAAATCTGGG AGGTGCTGGG AGTCCCTACA GAGGATACTT GGCCGGGAGT
1101 CTCCAAGCTA CCTAACTACA ATCCAGGTAA TATTGATCTG AGCTTTTGAA
1151 TACTCTGAGA ATTAGTAATG TAAGGAGAGC ATTGGCCACG CTAACAGGGC
1201 GTTCTTGTAT TGTGAACTCA GCGGCAAAGA TGGGTGTAGA GGAATTTCTA
1251 CATTCAATAA TTCCCTGACT AATCTTTGTA TGAGGAAGAC ACTGAAAGAG
1301 TAGCTGAGGT TAGACCAGTT CCCAGCTCT GTAAAACACA AGTAGCAAGC
1351 TGAATAGAAT TTGAAATGAC TATTACTGTG GATTCCACAT CCATTGTCAA
1401 ATACCCAATG GTCAAAAGA ACAACTCAAA AGATGGGCTC ACTTTTGGGC
1451 CCCCTGACTG TCATAAGTGT ATTGATTAGT ATTGAATTGC ATATGTATAA
1501 AAAGAAAGCT AATGCAACAG AACAGAGGTA GAGGCTCGCT AGGCCTAGGA
1551 CATGCCAAGT AAGCTGTCTG TAGGTTATAC TTAATAAGAG TTCATTCA T
1601 GCCTGTAAAC CTGACACTTG GTCATTGTCT CTCACACATT TCATCTTTCA
1651 AGACTGGCTT CTGGGATCGA TTTAGAAAGT CTGGAAGTGT TATCCATGGG
1701 GGAATTCTTT GAGAAGCTGT CGCAGGGCCA CATCAGAGGG ATCAGATTAA
1751 GCAGTAGTCA CTTCAAGGAT GTTGAGACAG AGGGGAGGAG ACAGGCACTG
1801 AACTACAGGA TGAAGGATCA TATTAGAAGC TGAAGAAGCA AATAAAGCCC
1851 ATGCCAAAGC TGAGCTCTCA CTGGCAGGGT TGAAGGGGAG GTAGAAAGGT
1901 ACAGATAACG ACAAGATTAG GGTGGATATG CTCCAAGCCA GATTTTTCTA
1951 GTCTTTATGG TCTTACATTG TTCCATTACT AAAAATGAAA TCTTCCCAA
2001 TTGTTGTCTT TACTTTTTTT TTTTTTTTTT GAGATGGAGT TTTGCTCTTA
2051 TCGCCAGGC TGGAGTGCAG TGAGCCGAGA TTGCGCCACT GCATGTCCGC
2101 AGTCCGACCT GGGCGACAGA GCGAGACTCC GTCTCAAAAC TAAAAAATAA
2151 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2201 AAA (SEQ ID NO:1)
```

FEATURES:

5'UTR: 1-117
Start Codon: 118
Stop Codon: 1147
3'UTR: 1150

SPLICE FORM 2 (transcript sequence):

1 ATGGGTCAAG AGCTGTGTGC AAAGACTGTA CAGCCTGGAT GCAGCTGCTA

FIGURE 1A

```

51 CCATTGTTCA GAGGGAGGCG AGGCACACAG CTGTCCGAGG AGTCAGCCTG
101 AGACCACGGA GGCTGCGTTC AAGCTAACAG ACCTAAAAGA AGCATCATGT
151 TCCATGACTT CATTTACCCC CAGGGGACTT CAAGCTGCCC GTGCCAGAA
201 GTTCAAGAGT AAAAGGCCAC GGAGTAACAG TGATTGTTTT CAGGAAGAGG
251 ATCTGAGGCA GGGTTTTTTCAG TGGAGGAAGA GCCTCCCTTT TGGGGCAGCC
301 TCATCTTACT TGAACCTGGA GAAGCTGGGT GAAGGCTCTT ATGCCAGACT
351 TTACAAGGGG ATTACAGAA TAAATGGACA ACTAGTGGCT TTAAAAGTCA
401 TCAGCATGAA TGCAGAGGAA GGAGTCCCAT TTACAGCTAT CCGAGAAGCT
451 TCTCTCCTGA AGGGTTTGAA ACATGCCAAT ATTGTGCTCC TGCATGACAT
501 AATCCACACC AAAGAGACAC TGACATTCGT TTTTGAATAC ATGCACACAG
551 ACCTGGCCCA GTATATGTCT CAGCATCCAG GAGGGCTTCA TCCTCATAAT
601 GTCAGACTTT TCATGTTTCA ACTTTTGCGG GGCCTGGCGT ACATCCACCA
651 CCAACACGTT CTTACAGGG ACCTGAAACC TCAGAACTTA CTCATCAGTC
701 ACCTGGGAGA GCTCAAACTG GCTGATTTTG GTCTTGCCCG GGCCAAGTCC
751 ATTCCCAGCC AGACATACTC TTCAGAAAGT GTGACCCTCT GGTACCGGCC
801 CCCTGATGCT TTGCTGGGAG CCACTGAATA TTCCTCTGAG CTGGACATAT
851 GGGGTGCAGG CTGCATCTTT ATTGAAATGT TCCAGGGTCA ACCTTTGTTT
901 CCTGGGGTCTT CCAACATCCT TGAACAGCTG GAGAAAATCT GGGAGGTGCT
951 GGGAGTCCCT ACAGAGGATA CTTGGCCGGG AGTCTCCAAG CTACCTAACT
1001 ACAATCCAGA ATGGTTCCCA CTGCCTACGC CTCGAAGCCT TCATGTTGTC
1051 TGGAACAGGC TGGGCAGGGT TCCTGAAGCT GAAGACCTGG CCTCCCAGAT
1101 GCTAAAAGGC TTTCCCAGAG ACCGCGTCTC CGCCCAGGAA GCACTTGTTT
1151 ATGATTATTT CAGCGCCCTG CCATCTCAGC TGTACCAGCT TCCTGATGAG
1201 GAGTCTTTGT TTACAGTTTC AGGAGTGAGG CTAAGCCAG AAATGTGTGA
1251 CCTTTTGGCC TCCTACCAGA AAGGTCACCA CCCAGCCCAG TTTAGCAAAT
1301 GCTGGTGA (SEQ ID NO:4)

```

FEATURES:

Start Codon: 1
Stop Codon: 1306

Homologous proteins:

Top 10 BLAST Hits

Score E

SPLICE FORM 1:

CRA 18000005115058	/altid=gi 6755044	/def=ref NP_035204.1	PFTA...	391	e-107
CRA 18000005205923	/altid=gi 6912584	/def=ref NP_036527.1	PFTA...	390	e-107
CRA 18000005100533	/altid=gi 2392814	/def=gb AAB70455.1	(U6239...	389	e-107
CRA 151000011260745	/altid=gi 12002201	/def=gb AAG43234.1	(AF1...	386	e-106
CRA 1000682315356	/altid=gi 5579351	/def=gb AAD45514.1	(AF1524...	367	e-100
CRA 89000000195020	/altid=gi 7292375	/def=gb AAF47781.1	(AE003...	367	e-100
CRA 1000682315355	/altid=gi 5579349	/def=gb AAD45513.1	(AF1524...	367	e-100
CRA 1000682315353	/altid=gi 5579343	/def=gb AAD45510.1	(AF1523...	367	e-100
CRA 1000682315354	/altid=gi 5579347	/def=gb AAD45512.1	(AF1524...	367	e-100
CRA 1000682315352	/altid=gi 5579341	/def=gb AAD45509.1	(AF1523...	367	e-100

SPLICE FORM 2:

CRA 18000005115058	/altid=gi 6755044	/def=ref NP_035204.1	PFTA...	469	e-131
CRA 18000005205923	/altid=gi 6912584	/def=ref NP_036527.1	PFTA...	468	e-131
CRA 18000005100533	/altid=gi 2392814	/def=gb AAB70455.1	(U6239...	467	e-131
CRA 151000011260745	/altid=gi 12002201	/def=gb AAG43234.1	(AF1...	465	e-130
CRA 1000682315356	/altid=gi 5579351	/def=gb AAD45514.1	(AF1524...	422	e-117
CRA 1000682315355	/altid=gi 5579349	/def=gb AAD45513.1	(AF1524...	422	e-117
CRA 1000682315354	/altid=gi 5579347	/def=gb AAD45512.1	(AF1524...	422	e-117
CRA 1000682315353	/altid=gi 5579343	/def=gb AAD45510.1	(AF1523...	422	e-117
CRA 1000682315352	/altid=gi 5579341	/def=gb AAD45509.1	(AF1523...	422	e-117
CRA 18000005045994	/altid=gi 1524004	/def=emb CAA67862.1	(X995...	421	e-116

FIGURE 1B

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

BLAST dbEST hits:

Score	E
SPICE FORM 1:	
gi 9806331 /dataset=dbest /taxon=960...	1334 0.0
gi 2140968 /dataset=dbest /taxon=9606 ...	575 e-162
gi 2028058 /dataset=dbest /taxon=9606 ...	377 e-102
gi 13132599 /dataset=dbest /taxon=960...	319 8e-85

FIGURE 1C

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

SPLICE FORM 2:

gi 9806331 /dataset=dbest /taxon=960...	1334	0.0
gi 2140968 /dataset=dbest /taxon=9606 ...	954	0.0
gi 2028058 /dataset=dbest /taxon=9606 ...	377	e-102
gi 2140870 /dataset=dbest /taxon=9606 ...	283	5e-74

EXPRESSION INFORMATION FOR MODULATORY USE:

SPLICE FORM 1:

library source (from BLAST dbEST hits):

gi|9806331 Uterus-endometrium adenocarcinoma cell line
gi|2140968 testis
gi|2028058 Lung fibroblast cell line
gi|13132599 kidney renal cell adenocarcinoma

Tissue Expression:

whole brain

SPLICE FORM 2:

library source (from BLAST dbEST hits):

gi|9806331 Uterus endometrium adenocarcinoma line
gi|2140968 Testis
gi|2028058 Lung fibroblast
gi|2140870 Testis

FIGURE 1D

SPLICE FORM 1:

```
1 MGQELCAKTV QPGCSCYHCS EGGEAHSCRR SQPETTEAAF KLTDLKEASC
51 SMTSFHPRGL QAARAQKFKS KRPRSNSDCF QEEDLRQGFQ WRKSLPFGAA
101 SSYLNLEKLG EGSYATVYKG ISRINGQLVA LKVISMNAEE GVPFTAIREA
151 SLLKGLKHAN IVLLHDIHT KETLTFVFY MHTDLAQYMS QHPGGLHPHN
201 VRLFMFQLLR GLAYIHHQHV LHRDLKPQNL LISHLGELKL ADFGLARAKS
251 IPSQTYSSEV VTLWYRPPDA LLGATEYSSE LDIWGAGCIF IEMFQGQPLF
301 PGVSNILEQL EKIWEVLGVP TEDTWPGVSK LPNYPGNID LSF (SEQ ID
NO:2)
```

SPLICE FORM 2:

```
1 MGQELCAKTV QPGCSCYHCS EGGEAHSCRR SQPETTEAAF KLTDLKEASC
51 SMTSFHPRGL QAARAQKFKS KRPRSNSDCF QEEDLRQGFQ WRKSLPFGAA
101 SSYLNLEKLG EGSYATVYKG ISRINGQLVA LKVISMNAEE GVPFTAIREA
151 SLLKGLKHAN IVLLHDIHT KETLTFVFY MHTDLAQYMS QHPGGLHPHN
201 VRLFMFQLLR GLAYIHHQHV LHRDLKPQNL LISHLGELKL ADFGLARAKS
251 IPSQTYSSEV VTLWYRPPDA LLGATEYSSE LDIWGAGCIF IEMFQGQPLF
301 PGVSNILEQL EKIWEVLGVP TEDTWPGVSK LPNYPNPEWFP LTPRSLHVV
351 WNRLGRVPEA EDLASQMLKG FPRDRVSAQE ALVHDYFSAL PSQLYQLPDE
401 ESLFTVSGVR LKPEMCDLLA SYQKGHHPAQ FSKCW (SEQ ID NO:5)
```

FEATURES:

Functional domains and key regions:

SPLICE FORM 1:

[1] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2

1	27-29	SCR
2	70-72	SKR

[2] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 3

1	31-34	SQPE
2	75-78	SNSD
3	279-282	SELD

[3] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

108-114 KLGEFSY

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1	2-7	GQELCA
2	59-64	GLQAAR
3	98-103	GAASSY
4	112-117	GSYATV
5	126-131	GQLVAL
6	141-146	GVPFTA
7	155-160	GLKHAN

FIGURE 2A

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

8 244-249 GLARAK

[5] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

109-132 LGEGSYATVYKGISRINGQLVALK

FIGURE 2B

[6] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

220-232 VLHRDLKPQNLLI

[7] PDOC00170 PS00191 CYTOCHROME_B5_1
Cytochrome b5 family, heme-binding domain signature

188-195 YMSQHPGG

SPLICE FORM 2:

[1] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 3

1	27-29	SCR
2	70-72	SKR
3	343-345	TPR

[2] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 4

1	31-34	SQPE
2	75-78	SNSD
3	279-282	SELD
4	377-380	SAQE

[3] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

108-114 KLGEFSY

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8

1	2-7	GQELCA
2	59-64	GLQAAR
3	98-103	GAASSY
4	112-117	GSYATV
5	126-131	GQLVAL
6	141-146	GVPFTA
7	155-160	GLKHAN
8	244-249	GLARAK

[5] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

109-132 LGEGSYATVYKGISRINGQLVALK

[6] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

FIGURE 2C

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

220-232 VLHRDLKPQNLLI

FIGURE 2D

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

[7] PDOC00170 PS00191 CYTOCHROME_B5_1
Cytochrome b5 family, heme-binding domain signature

188-195 YMSQHPGG

Membrane spanning structure and domains:

(SPLICE FORMS 1 & 2)

Helix	Begin	End	Score	Certainty
1	283	303	0.776	Putative

FIGURE 2E

BLAST Alignment to Top Hit:

SPLICE FORM 1:

>CRA|18000005115058 /altid=gi|6755044 /def=ref|NP_035204.1|
PFTAIRE

protein kinase 1 [Mus musculus] /org=Mus musculus
/taxon=10090 /dataset=nraa /length=469
Length = 469

Score = 391 bits (993), Expect = e-107
Identities = 184/240 (76%), Positives = 208/240 (86%)
Frame = +1

Query: 406

FGAASSYLNLEKLGEFSYATVYKGISRINGQLVALKVISMNAEEGVPFTAIREASLLKGL 585
FG A SY LEKLGEFSYATVYKG S++NG+LVALKVI + EEG

PFTAIREASLLKGL

Sbjct: 129

FGKADSYEKLEKLGEFSYATVYKGKSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 188

Query: 586

KHANIVLLHDIHTKETLTFFVEYMHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 765
KHANIVLLHDIHTKETLT VFEY+HTDL QYM QHPGGLHP

NV+LF+FQLLRGL+YIH

Sbjct: 189

KHANIVLLHDIHTKETLTFLVEYVHTDLCQYMEQHPGGLHPDNVKLFLFQLLRGLSYIH 248

Query: 766

HQHVLHRDLKPQNLLISHLGELKLADFGGLARAKSIPSQTYSSSEVTLWYRPPDALLGATE 945
+++LHRDLKPQNLLIS GELKLADFGGLARAKS+PS TYS+EVVTLWYRPPD

LLG+TE

Sbjct: 249

QRYILHRDLKPQNLLISDTGELKLADFGGLARAKSVPSHTYSNEVTLWYRPPDVLLGSTE 308

Query: 946

YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPN 1125
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV

LP++ P

Sbjct: 309

YSTCLDMWGVGCIFVEMIQGVAAFPGMKDIDQLERIFLVLGTPNEDTWPGVHSLPHFKP 368
(SEQ ID NO:6)

>CRA|18000005205923 /altid=gi|6912584 /def=ref|NP_036527.1|
PFTAIRE

protein kinase 1 [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=451
Length = 451

Score = 390 bits (990), Expect = e-107
Identities = 184/245 (75%), Positives = 209/245 (85%)
Frame = +1

Query: 406

FGAASSYLNLEKLGEFSYATVYKGISRINGQLVALKVISMNAEEGVPFTAIREASLLKGL 585

FIGURE 2F

Docket No.: CL001098DIV II
Serial No.: TO BE ASSIGNED
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN KINASE ...

FG A SY LEKLGEGSYATVYKG S++NG+LVALKVI + EEG
PFTAIREASLLKGL
Sbjct: 111
FGKADSYEKLEKLGEGSYATVYKGKSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 170

Query: 586
KHANIVLLHDIHTKETLTFVFEYMHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 765
KHANIVLLHDIHTKETLT VFEY+HTDL QYM +HPGGLHP
NV+LF+FQLLRGL+YIH
Sbjct: 171
KHANIVLLHDIHTKETLTLVFEYVHTDLCQYMDKHPGGLHPDNVKLFLFQLLRGLSYIH 230

Query: 766
HQHVLHRDLKPQNLLISHLGELKLADFGGLARAKSIPSQTYSSSEVVTWYRPPDALLGATE 945
+++LHRDLKPQNLLIS GELKLADFGGLARAKS+PS TYS+EVVTWYRPPD
LLG+TE
Sbjct: 231
QRYILHRDLKPQNLLISDTGELKLADFGGLARAKSVPSHTYSNEVVTWYRPPDVLLGSTE 290

Query: 946
YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYP 1125
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV
LP++ P
Sbjct: 291
YSTCLDMWGVGCIFVEMIQGVAAFPGMKDIQDQLERIFVLGTPNEDTWPGVHSLPHFKP 350

Query: 1126 GNIDL 1140
L
Sbjct: 351 ERFTL 355 (SEQ ID NO:7)

SPLICE FORM 2:
>CRA|18000005115058 /altid=gi|6755044 /def=ref|NP_035204.1|
PFTAIRE
protein kinase 1 [Mus musculus] /org=Mus musculus
/taxon=10090 /dataset=nraa /length=469
Length = 469

Score = 469 bits (1195), Expect = e-131
Identities = 225/330 (68%), Positives = 270/330 (81%)

Query: 97
FGAASSYLNLEKLGEGSYATVYKGISRINGQLVALKVISMNAEEGVPFTAIREASLLKGL 156
FG A SY LEKLGEGSYATVYKG S++NG+LVALKVI + EEG
PFTAIREASLLKGL
Sbjct: 129
FGKADSYEKLEKLGEGSYATVYKGKSKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGL 188

Query: 157
KHANIVLLHDIHTKETLTFVFEYMHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 216
KHANIVLLHDIHTKETLT VFEY+HTDL QYM QHPGGLHP
NV+LF+FQLLRGL+YIH
Sbjct: 189
KHANIVLLHDIHTKETLTLVFEYVHTDLCQYMEQHPGGLHPDNVKLFLFQLLRGLSYIH 248

FIGURE 2G

Query: 217
HQHVLHRDLKPQNLLISHLGELKLADFLARAKSIPSQTYSSSEVVTLWYRPPDALLGATE 276
+++LHRDLKPQNLLIS GELKLADFLARAKS+PS TYS+EVVTLWYRPPD

LLG+TE
Sbjct: 249
QRYILHRDLKPQNLLISDTGELKLADFLARAKSVPSHTYSNEVVTLWYRPPDVLLGSTE 308

Query: 277
YSSELDIWGAGCIFIFEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPN 336
YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV

LP++ P
Sbjct: 309
YSTCLDMWGVGCIFVEMIQGVAAFPGMKDIQDQLERIFVLGTPNEDTWPGVHSLPHFKP 368

Query: 337
EWFPLPTPRSLHVWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQ 396
E F + + +SL WN+L V AEDLAS++L+ P++R+SAQ AL H+YFS

LP +L++
Sbjct: 369
ERFTVYSSKSLRQAWNKLSYVNHAEADLASKLLQCSPKNRLSAQAALSHEYFSDLPRLWE 428

Query: 397 LPDEESLFTVSGVRLKPEMCDLLASYQKGH 426

L D S+FTV VRL+PE + + ++ K +
Sbjct: 429 LTDMSSIFTVPNVRLQPEAGESMRAFGKNN 458 (SEQ ID NO:8)

>CRA|18000005205923 /altid=gi|6912584 /def=ref|NP_036527.1|
PFTAIRES
protein kinase 1 [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=451
Length = 451

Score = 468 bits (1191), Expect = e-131
Identities = 224/330 (67%), Positives = 270/330 (80%)

Query: 97
FGAASSYLNLEKLGEFSYATVYKGISRINGQLVALKVISMNAEEGVPFTAIRESLLKGL 156
FG A SY LEKLGEFSYATVYKG S++NG+LVALKVI + EEG

PFTAIRESLLKGL
Sbjct: 111
FGKADSYEKLLEKLGEFSYATVYKGKSKVNGKLVALKVIRLQEEEGTPFTAIRESLLKGL 170

Query: 157
KHANIVLLHDIHTKETLTFVFEYMHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIH 216
KHANIVLLHDIHTKETLT VFEY+HTDL QYM +HPGGLHP

NV+LF+FQLLRGL+YIH
Sbjct: 171
KHANIVLLHDIHTKETLTLVFEYVHTDLCQYMDKHPGGLHPDNVKLFLFQLLRGLSYIH 230

Query: 217
HQHVLHRDLKPQNLLISHLGELKLADFLARAKSIPSQTYSSSEVVTLWYRPPDALLGATE 276
+++LHRDLKPQNLLIS GELKLADFLARAKS+PS TYS+EVVTLWYRPPD

LLG+TE
Sbjct: 231
QRYILHRDLKPQNLLISDTGELKLADFLARAKSVPSHTYSNEVVTLWYRPPDVLLGSTE 290

FIGURE 2H

Query: 277
 YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYP 336
 YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV
 LP++ P
 Sbjct: 291
 YSTCLDMWGVGCIFVEMIQGVAAFPGMKDIQDQLERIFLVLGTPNEDTWPGVHSLPHFKP 350

Query: 337
 EWFPLPTPRSLHVWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQ 396
 E F L + ++L WN+L V AEDLAS++L+ P++R+SAQ AL H+YFS
 LP +L++
 Sbjct: 351
 ERFTLYSSKNLRQAWNKL SYVNHAEDLASKLLQCSPKNRLSAQAALSHEYFSDLPPRLWE 410

Query: 397 LPDEESLFTVSGVRLKPEMCDLLASYQKGH 426
 L D S+FTV VRL+PE + + ++ K +
 Sbjct: 411 LTDMSSIFTVPNVRLQPEAGESMRAFGKNN 440 (SEQ ID NO:9)

>CRA|18000005100533 /altid=gi|2392814 /def=gb|AAB70455.1|
 (U62391)
 PFTAIRE kinase [Mus musculus] /org=Mus musculus
 /taxon=10090 /dataset=nraa /length=423
 Length = 423

Score = 467 bits (1190), Expect = e-131
 Identities = 224/330 (67%), Positives = 269/330 (80%)

Query: 97 FGAASSYLNLEKLGEFSYATVYKGISRINGQLVALKVISMNAEEGVPFTAIREASLLKGL 156
 FG A SY LEKLGEFSYATVYKG S++NG+LVALKVI + EEG PFTAIREASLLKGL
 sbjct: 83 FGKADSYEKLLEKLGEFSYATVYKGKSKVNGKLVALKVIRLQEEGTPFTAIREASLLKGL 142

Query: 157 KHANIVLLHDIIHTKETLTTFVEYMHDTLAQYMSQHPGGLHPHNVRFLMFQLLRGLAYIH 216
 KHANIVLLHDIIHTKETLT VFEY+HTDL QYM +HPGGLHP NV+LF+FQLLRGL+YIH
 sbjct: 143 KHANIVLLHDIIHTKETLT VFEYVHTDLCQYMDKHPGGLHPDNVKLFLFQLLRGLSYIH 202

Query: 217 HQHVLHRDLKPQNLLISHLGELKLADFLARAKSIPSQTSSEVVT LWYRPPDALLGATE 276
 +++LHRDLKPQNLLIS GELKLADFLARAKS+PS TYS+EVVT LWYRPPD LLG+TE
 sbjct: 203 QRYILHRDLKPQNLLISDTGELKLADFLARAKSVPSHTYSNEVVT LWYRPPDVLLGSTE 262

Query: 277 YSSELDIWGAGCIFIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYP 336
 YS+ LD+WG GCIF+EM QG FPG+ +I +QLE+I+ VLG P EDTWPGV LP++ P
 sbjct: 263 YSTCLDMWGVGCIFVEMIQGVAAFPGMKDIQDQLERIFLVLGTPNEDTWPGVHSLPHFKP 322

Query: 337 EWFPLPTPRSLHVWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQ 396
 E F + +SL WN+L V AEDLAS++L+ P++R+SAQ AL H+YFS LP +L++
 sbjct: 323 ERFTVYNSKSLRQAWNKL SYVNHAEDLASKLLQCSPKNRLSAQAALSHEYFSDLPPRLWE 382

Query: 397 LPDEESLFTVSGVRLKPEMCDLLASYQKGH 426 L D S+FTV VRL+PE + + ++ K +
 Sbjct: 383 LTDMSSIFTVPNVRLQPEAGESMRAFGKNN 412 (SEQ ID NO:10)

FIGURE 2I

Hammer search results (Pfam):

SPLICE FORM 1:

Model	Description	Score
E-value	N	
PF00069	Eukaryotic protein kinase domain	247.7
1.6e-70	1	
CE00031	CE00031 VEGFR	14.3
0.0002	1	
CE00359	E00359 bone_morphogenetic_protein_receptor	7.1
0.25	1	
CE00022	CE00022 MAGUK_subfamily_d	6.0
0.11	1	
CE00287	CE00287 PTK_Eph_orphan_receptor	-59.4
0.00019	1	
CE00292	CE00292 PTK_membrane_span	-61.0
1.9e-05	1	
CE00286	E00286 PTK_EGF_receptor	-76.4
1.9e-06	1	
CE00291	CE00291 PTK_fgf_receptor	-87.0
0.00095	1	
CE00290	CE00290 PTK_Trk_family	-100.0
1.4e-08	1	
CE00016	CE00016 GSK_glycogen_synthase_kinase	-152.6
3.5e-08	1	
CE00288	CE00288 PTK_Insulin_receptor	-196.5
0.0012	1	

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/1	204	231 ..	126	153 ..	6.0	0.11
CE00359	1/1	222	247 ..	274	299 ..	7.1	0.25
CE00031	1/1	204	247 ..	1051	1094 ..	14.3	0.0002
CE00290	1/1	106	307 ..	1	282 []	-100.0	1.4e-08
CE00288	1/1	106	310 ..	1	269 []	-196.5	0.0012
PF00069	1/1	103	326 ..	1	220 []	247.7	1.6e-70
CE00286	1/1	103	335 ..	1	263 []	-76.4	1.9e-06
CE00287	1/1	104	335 ..	1	260 []	-59.4	0.00019
CE00016	1/1	1	340 []	1	433 []	-152.6	3.5e-08
CE00292	1/1	104	341 ..	1	288 []	-61.0	1.9e-05
CE00291	1/1	104	341 ..	1	285 []	-87.0	0.00095

FIGURE 2J

SPLICE FORM 2:

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	263.6	2.6e-75	1
CE00031	CE00031 VEGFR	14.3	0.0002	1
CE00359	E00359 bone_morphogenetic_protein_receptor	7.1	0.25	1
CE00022	CE00022 MAGUK_subfamily_d	6.0	0.11	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-42.5	3.2e-14	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-55.2	0.0001	1
CE00292	CE00292 PTK_membrane_span	-63.9	2.8e-05	1
CE00286	E00286 PTK_EGF_receptor	-76.4	1.9e-06	1
CE00291	CE00291 PTK_fgf_receptor	-88.8	0.0012	1
CE00290	CE00290 PTK_Trk_family	-94.9	6.1e-09	1
CE00288	CE00288 PTK_Insulin_receptor	-196.5	0.0012	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/1	204	231 ..	126	153 ..	6.0	0.11
CE00359	1/1	222	247 ..	274	299 ..	7.1	0.25
CE00031	1/1	204	247 ..	1051	1094 ..	14.3	0.0002
CE00288	1/1	106	310 ..	1	269 []	-196.5	0.0012
CE00286	1/1	103	335 ..	1	263 []	-76.4	1.9e-06
CE00292	1/1	104	335 ..	1	288 []	-63.9	2.8e-05
CE00291	1/1	104	339 ..	1	285 []	-88.8	0.0012
CE00290	1/1	106	354 ..	1	282 []	-94.9	6.1e-09
CE00287	1/1	104	367 ..	1	260 []	-55.2	0.0001
PF00069	1/1	103	387 ..	1	278 []	263.6	2.6e-75
CE00016	1/1	1	434 []	1	433 []	-42.5	3.2e-14

FIGURE 2K

1	TATAGGCCAA	TGCTGTGGCT	CACGCGTGTA	TTCCCAGCAC	TTTGGGAGGC
51	AGGAGGATCG	CTTGAGCTCA	GGAATTGGAG	ACAAGCCTAC	GTAACATAGT
101	GAAACCTCTG	TCTGTACAAA	TAATAAAAGA	ATTTTCCAGG	CATGGTGGCG
151	TGCACCCCCA	GTGCCAGCTA	TTTGGGAGGC	TGAGGTAGGA	GGAATGCTTG
201	AAGCCAGGAG	TTGAAGACAA	GCCTAGGCAA	CATAGTGAGA	CCCTGTGTCT
251	ATAAAAAATA	ATTAGCTGGT	TGTCTTGCCA	CAGGCCTGCA	GCTAGCTACT
301	CGGAAGACTG	AGGTGGGAGG	ATCACTGAGC	CCAGGAGGCT	GAGGCTGCAG
351	TGAACAGTGA	TCACCCAGCT	GGATTCCAGC	CTGGAAGACA	GAGGGAGACC
401	CTGTTTCCAA	AAAAAAAAAA	AAAAAAAAAAT	GCAAGAAAAG	ACATCATAAA
451	CTTGACCTGG	GACATAACTT	TTATGTGATG	AAATTCACAA	TCTTTTAGGA
501	AGAAATTAGC	ATTTCTGATA	AAATGTATTA	TAATTATATT	ATTATAAATT
551	CAAATGGAAT	TAAATATTCT	GAGAACTAG	CTTCTCACTC	TCTCAGTTGT
601	CAGTCAAAAC	TTTAATGGTC	TTTGGCCGGG	TGCGGTGGCT	CACGCCTGTA
651	ATCCCAGCAC	TTTGGGAGGC	CGAGGCGGGT	GGATCACAAG	GTTAGGAGAT
701	CGAGACCATC	CTGGCTAACA	CGGTGAAACC	TCGTCTCTAC	TAAAAATACA
751	AAAAATTAGC	CGGGTGCGGT	GCCAGACGCC	TGTAGTCCCA	GCTGCTCAGG
801	AGGCTGAGGC	AGGAGAAATG	TGTGAACCCG	GGAGGCGGAG	CTTGCACTGA
851	GCCGAGATTG	CGCCACTGCA	CTCCAGCCTG	GGCGACAGTG	CGAGACTCTG
901	TCTCAAAAAA	AAAAAAAAAA	AAAAGTTGAA	TGGTCTTTGA	GCCAAGTAGT
951	CTTCCTTTTC	TTCTTCTTCT	TTTTTTTTTT	TTTTCAAAAA	ATATCTCTAG
1001	ATTGAATCTT	GGAATTGGCT	TAAGTCTCTT	CTCTTGTGGC	AATTTTGAAA
1051	TGAAAAAATA	CATGCTCATA	ATTAAATTAC	CTGAACATTT	TAAAAAACCA
1101	TCATGAGGTT	CAAATATCAA	ATATTCATAA	ATATTGTTGT	GATAATAGAC
1151	ATAACTCTTA	TTTTTTCCTT	TAATAATGAT	TGTTTATATA	TCCTCCATTC
1201	TGTCTCACTT	TATGATTAGT	ATATTATAGT	GGCAATAATC	TTAGGAATCT
1251	AACAGAGAAA	AGTGTGTCAT	TTGAAGACTA	CAGACTGCAA	ACCAATTTAA
1301	GCCAGATTCC	TTGACATGTT	GTGCTGTAA	TATAGTACTT	TACATATAGT
1351	AAACATTAAT	TACATATATG	TGGAAGGAAG	CAAGCAAGAA	AGGAAGAAAAG
1401	TATTTCAATC	AAACTCCTCT	CTCTCCATCA	CCATTGGCTA	ATATCATCAT
1451	TTGTACAGTT	AAGAACAACA	TAGGTGCTCA	CCACATAGTT	TTTGAATAAA
1501	TGAATGAATG	GCAACCCTTC	TAAGACTATT	GGATACACTA	TTGTTTGAAG
1551	GCAAAGAGAT	GCAGTAGATA	TTTTCAACTT	TTTTCTGTGT	TTATGATTCT
1601	GTGGTTTCTT	TGACTACTAA	AAGTTAGCTA	GGTAGCAAAT	TTGTTTTTAA
1651	GTCTGAAAAC	CAAAATGCTT	TCAGATAAAA	GGTAGGGAGA	AAAATACTCC
1701	TCAACATGTC	CACTTTAGCA	CCAGGAAAAC	CTAATATCAA	TATCACCATC
1751	AATGATATCA	TATAAATATC	ATTGCATAGA	TAAGCAATGT	CAATCCCTAA
1801	AAACTATGTA	TACCAATAGC	ACTAACTTGT	GGCCAGAACA	AGAACCTTAA
1851	CTGTGCCAAA	TTTTATTCTA	TTCAATAACA	GCTGCCTCGT	TTTCAGTTGT
1901	GCACATCTGA	ATGCAAGCAA	TCCCTGTCTG	ATGTGGAGTT	TCTTGCACTG
1951	ATAAGGAAAA	ACTGCTGAAG	TTGTGAGGCT	GCTCCAGGCA	GAGCCATCAT
2001	GTGAGTCATA	TGAAAGCTCC	ACGCTGCTGA	CCTCTGGCAA	AAAGGGAGAG
2051	AACAAGGATA	GGAGAGGCAG	TGGGGGAAAG	GTTCAAGTGC	GGGTTTTCTC
2101	CTTGAACCTA	CAAGATTATG	GGTCAAGAGC	TGTGTGCAAA	GACTGTACAG
2151	CCTGGATGCA	GCTGCTACCA	TTGTTTCAAG	GGAGGCGAGG	CACACAGCTG
2201	TCGGAGGAGT	CAGCCTGAGA	CCACGGAGGC	TGCGTTCAAG	GTATTTGTAT
2251	CCCAGGAGAG	AGCATCTTTC	TCTATTGATA	AACCAAGGAG	TTCAGACACT
2301	CCCTTTTTGT	AGCGGGATCT	GATTCTTCTG	CGGTAGGTCT	AAACCAATAA
2351	AATGAAAATT	CTATTAAAGT	CACAGAAAAT	TTATGGCTGT	AGTTATCAAA
2401	TTTGGGGAAT	TTCTTGTAAG	CCAAAAGGGA	AAAATAATCC	TTGGCTTTGG
2451	GCTGCACGAA	ACTCACTTGG	CTTGAAGTCG	AGAAAGTAGT	TCTCTCAAAA
2501	TCTCTAAGGT	CCTAAATTAC	AGAGCTGAAA	CTTAAAAGGC	AAGCTGCAGT
2551	ATTAGTTGGT	ATGCTATGGA	TTTGAAACTT	TAGTAATTAG	TTCATGATTA
2601	TTAGCAATGC	CATAGATTAT	TCCCCTACAG	CAATAAATTA	AGTGGACATG
2651	AAAAAAAAAA	GCCAGACTTA	AACAGAAAAA	AGTTGCAAAA	CATCCATCAA
2701	AGAGATTTAG	GTTAACCTGA	ATGTTAAAGA	CACATTTTTA	GGTGAAGAAA

FIGURE 3A

2751	GAATGTAGTA	TTTCAGGAGT	TGATACCATT	ATGGTCTTTT	TCAGGGATCT
2801	TTCAAGAAAA	GTGCCTTTTG	GGGGTACAGG	AAGCTTAGAA	AACATTTGAA
2851	GAGTGAAAA	GAGGCAAATA	AAGAAAAAAT	GGTTTTACCA	GGCACTGAAT
2901	CTTTACTTTG	CATAAATTTT	ATTTCTGCTC	TTTCTTTTTT	CTCTAGCTAA
2951	CAGACCTAAA	AGAAGCATCA	TGTTCCATGA	CTTCATTTCA	CCCCAGGGGA
3001	CTTCAAGCTG	CCCGTGCCCA	GAAGTTCAGG	AGTAAAAGGC	CACGGAGTAA
3051	CAGTGATTGT	TTTCAGGAAG	AGGATCTGAG	GCAGGGTTTT	CAGTGGGTGA
3101	GTGAGCAGCT	GATGTTGATC	AAGAAGAATT	TAATGTGAGC	TTGTCTACGG
3151	AGGCCGGCCC	TTGCTTCCAG	GGCAATTACT	GAGCGAGCCT	TCCCAAGTCT
3201	GCTCTGGCAA	TGCTGTCTAA	TTTCCCTGGG	GAAAAAAAGT	CAACACTAAA
3251	AAAAAGTGTT	CTTTCTCTCT	TCCCTTTTAC	CCGCTCCTTT	TCCCCATTCC
3301	CCTAGAGCAG	AGGAAGAGCC	TCCCTTTTGG	GGCAGCCTCA	TCTTACTTGA
3351	ACTTGGAGAA	GCTGGGTGAA	GGCTCTTATG	CGACAGTTTA	CAAGGGGATT
3401	AGCAGGTGAG	TGACACATAG	CTGGGAGAGA	CTTTAGAGAT	GAGAGTCCCG
3451	CCCCCCCCAAT	TTCATATTAT	AAAGCCAGGT	GAGACATCAT	AGAAGTTCAT
3501	AGCACTCAGG	ACCTGTGCAA	GACACCATGG	CCGACAGGGA	GAGAGACATG
3551	ATAACTTAAA	CAGCCTTGAA	AGAAAAACAA	ACCTGCCCTG	CCCTAATTAA
3601	AATCAGCCCA	CTTAAATGTT	TATCAGCCTT	TCCCTTCTTG	CATTCAATTC
3651	AGAGAATTCA	AAGAAAAATAG	ACATTCTCTA	CTACTGACCC	AAAGAACAAT
3701	TATCACTCTT	CAGGCCTGTG	GGAGGCACAG	TTGGTAAAGC	GTCTCTAACA
3751	GGTTTTTTTAT	ATCCCTCCCT	AAATCACAAT	GACAGAGTTT	TGTAATGGCA
3801	ACCTGGAATT	TGCTGCTTCA	TTCTCCACC	TGGCCTTTAT	AGAAGAACT
3851	GAAGTTGGTT	TCTGCAAATT	ATGGTACATG	CAAAAGATGA	TAAATCCTAG
3901	ATTTTTTATA	TTTGCAAAAT	ACACAAAATG	TCTGGAGAAT	AAAAATACTG
3951	CTTATCCAAA	AGCTAAGTAC	TAATTTTGGT	AAACAACCAA	CTTTGTTAAA
4001	TATATGTAAA	AGATCCATGA	ATTCCCCTTT	TAGTCAAGGT	GGGAAAGTTG
4051	GATGGTCGCT	TTTTTCTTTA	TGTTACTCCA	ATAGAGAGAA	AAGTAATGGC
4101	TCAATAGTGG	TTAAATATTA	ATTTTAAAAA	TATAGCTGAT	CCGAGTGCAG
4151	TGGTGTTTAC	AACTACTTGA	TCACAACCAG	TTACAGATTT	CTTTGTTTCT
4201	TCTCCATCTC	CCTGCTTCA	CTTAACTGGC	CAAAAACGAA	AAAAGAAAAA
4251	TTTTATATAA	CTACTACAAG	ACTAAATATT	TATTATTTAT	CTTAGTATTT
4301	ATGCTGTTAT	TATTATTTTT	ACTTGTTAAA	ACAGGATTGT	AGGGGACATA
4351	CAGTTTTATT	TTATTTTATT	ATTTATATAT	TTATTTATTT	ATTTTGGAAT
4401	GGAATCTCTG	TCACCCACGC	TGGAGTGCAG	TGGTGCGATC	TCAGATGACT
4451	GCAACCTCTG	CCTCCTGAGT	TCAAGCAACT	CTCCTGCCCC	TGGCCCTTTA
4501	TACTTTCTTA	ATCTGTTTTA	GTCATGGTGT	ACCTTAACTT	TTTTCAATGC
4551	TGAGAACATC	TGCAATAAAG	GACCACATTT	TATTTTATTC	TAAGCTTCCT
4601	CATATCAATT	TGGCCATGGT	AACTGTTTTT	AAGGTGGCTC	GGAACGGGGG
4651	CACCCTGGAA	CATACTTGGA	TACATGGGCA	CCATGGACAC	TTCTGATCCT
4701	CTCTTCTGAG	TTCTGACTTT	GATTGTTCTG	CACAGACCTT	TCCAGCCCCG
4751	AGTTTACACA	GAATTCACTT	ATCTTTTCTT	CTAGTTACTT	TATGTTTTCT
4801	TTTTCATTTA	ACTCTTTCAT	CTACTGGGAA	TTTATATTGT	ATATTCACAA
4851	TCACCCCAGC	TCCATTTATT	AGATTTTCTT	TTCTCTGATG	GTTTGAAATG
4901	CTGCCATGAT	TATATATTAG	ATCTCACGAA	TACTTGAAAT	TCTTTCTGTT
4951	CTAATCTTTT	AAAAATCATG	TTTCCTTAAT	CTATCTTTTC	TTATATTTGT
5001	GCTGCATGAT	TTTAATTATT	GTTGCTTTAG	GCTATTTTTA	GAATATATCA
5051	AAACTCTACG	TTAGAGAATT	ATTGACATCT	TTGCATTATT	AGATTTTCTA
5101	ATACAAATAT	CCTGTAAATA	TCTAATACAA	CAGTCTCTGG	ATGGTCACTG
5151	TACAAGACCC	TATAGAATCC	CTACCCTCCA	TTCCCCGGCA	CACACTCAGC
5201	TCCTCCCTGT	CCTCATCTCC	TTCCCCTCTC	CTGCTTCAAT	GACAGACTGC
5251	TCCTGCCTCA	GTCAAGGACT	TTTAACTTGC	TGTTCCCTCT	GCCTGGAGCT
5301	GCCTTCCACT	GTTTCATGCAC	ACAGCTGACT	CCCCCTCGCC	ATCAGATTCC
5351	TGGTTCAAGT	GTTACCTTAT	TTATAAACT	GTAGTCCCAG	CTAGTCCAGG
5401	GAGGCTGGAG	GCAGGAGAAT	CACCTTGAAC	TTGGAGGCAG	AGGTTGCAGT
5451	GAGCTGAGAT	CGGCACCACC	GCACTCCAGC	CTGGGTGAGA	GTGACACTGT

FIGURE 3B

5501	CTCAAAAAA	AAAAAAGCA	TTTTCTCTTA	TAAACATATT	TGCCAAAAA
5551	CTTTTTGCAG	GGTTTGGGG	AGAATTTTAC	AGAACCATGT	TCTGAGGAAA
5601	ATACTTACCT	CATAAACTC	TAAAACAAAA	TTTCAAAGAC	ATGATAAGGC
5651	AAACAAAAGA	AACTGGGGAA	AAGTATATGC	AAAATAGTTC	AATAAAAAGG
5701	TGGGCAAATC	GGCAAATCAC	AAGAAAAACA	GAAAAGATCC	ATAAACTTAT
5751	GAAAAGTCAG	TTTCACATAT	GGTTAAAGAA	ATATAAATTA	AAATGCGATA
5801	AACCTTTTTA	CTTTTCAAAT	AGGCCAAAAA	AAAAAAGAAG	ATGAAAGCGA
5851	AAAGCCAACC	CACATGATAG	GGCTATGACA	GAGGGACACA	GGAGCCAAC
5901	GAAAGAGCTT	CCAAAGGACA	AAGCTGCAAA	AATATGAGCA	ACCAAAAAA
5951	GTGGTATTAA	ATTATAACCC	AAAGTATAAA	ATAAATATCT	ATGAGTCCGT
6001	ACTGATATAA	ATAAATGATT	CAATACATTA	ACAAATGGGA	GAGAAGAAAC
6051	AAATCTCTCA	TGCCAAATAA	ATACAAATAA	TTTATGTAGA	TAATATACCT
6101	TCAAAGAGGT	ACAGCATAAC	TCTCCACTCC	TTAAGTGTGG	GTCATTCATA
6151	GTGGCATTTC	TCTAAAAGTA	CAGTATGAAA	AAGGGGGAGA	AAGAGTAACT
6201	TTAGAGTAGA	GAAACCTGAC	CAACACTATC	TCAGACAGGT	GACTAAGGTC
6251	AACATCAAAA	GTCATAAATC	ATGATGATGG	TATGCACTCT	TTTTTTTTTT
6301	TTTTTTTTTT	TTCTCAGATG	GAGTCTCACT	CTGTCGCCCC	GGCTGGGGTG
6351	CAGTGGCGCA	ATCTCAGCTC	AGTCCAACCT	CCGGCTCCCG	GGTTCAAGCG
6401	ATTCTCCTCT	CAGCCTCCTG	AGTAGCTGGG	ATCACAGGCG	CGTGCCACCA
6451	TACCCGGCTA	ATTTTTTGTA	TTTTAGTAGA	GACGGGGTTT	CACCATGTTG
6501	CCCAGGCTGG	TCTCAAACCTC	CCGAGCTCAG	GCAATCCACC	CACCTCAACC
6551	TCCCAAAGTG	CTAGGATTAC	AGGCATGAGC	CACTGCGCCT	GGCTGAGGGT
6601	ATGCACTTTT	TTTTTTTTTTG	AGACGGAGTC	TTGCTCTGTC	GCCCAGGCTG
6651	GAGTGCAGTG	GCACGATCTT	GGCTCACTGC	AAGCTCCGCC	TCCCAGGTTT
6701	ACGCCATTCT	CCTGCCTCAG	CCTCCCCAGT	AGCTGGGACT	ACAAGGTGCC
6751	CCACCACCCA	CACCCGGCTA	ATTTTTTGTA	TTTTTAGTAG	AGACGGGGTT
6801	TCAGTGTGTT	AGGCAGGATG	GTCTCGATCT	CCTGACCTCC	TGATCCACCG
6851	GCCTTCGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTGAGCC	ACTGTGCCCC
6901	GCCTGATGAA	ATGTTAAATC	TTTATTAAT	ATCGGATTGT	ACAAGAATGA
6951	ACTATAAGAG	AAAAGTTACA	TGGAGGAAAA	AAGGTTACTA	ACAATTAATGA
7001	TTTAATCCCA	CTGTATTAAA	AACAATGGAT	TTATACCTGC	ATTAAAATCT
7051	TCTCTATTCT	CAGCACTTAG	CTGATATGAA	TAAAATGATG	AATGAGGGGA
7101	CAGTAGGAGG	AAATGAAGAG	AGAGAGAATA	ATGGTGTGGC	CTGGGAAGAT
7151	CAGGTAGCAC	TTAGAAGCCC	GCTGCAAGAA	TTTGGCTTTT	ATTCTAAGTA
7201	ATGCGTGGAG	ATATGGTGGC	TTTTGAACAG	AAAAGTGACT	TGTCCTGATT
7251	GTCATTTGAA	AAGTATGCCT	CCAACACTA	CTGCTGAGAG	TAAATAGTAG
7301	GAGTGCAAGT	GTGCTCAGCA	GGGAAACTGT	TAGAAGACCA	CTACAAGGCT
7351	GGGCTTGGTG	GCTCGTGCCT	GTAATCCCAG	CACTTTGGGA	GCCTGACGTG
7401	GGCAGATCAC	CTGAGGTCAG	GAGTTCGAGA	CCAGCCTGGC	CAAAATGGTG
7451	AAACCCCAT	CTCTGCTAAA	AATACAAAAA	TTAGCCAGGT	GTGGTGGGGG
7501	TCCCCTGTAA	TCCCAGCTTC	TTGGGAGGCT	GAGGCAGGAG	AATTGCTTGA
7551	ACCCAGGAGG	TGGAGGTTGC	AGTGAGCCAA	GATCGTGCCA	CTGTACTCCA
7601	GCCTGGGCAA	CAGAGCGAGA	TTCTGTCTCA	AAAAAATAAA	AAAAAACA
7651	AAAAACAATA	AAACACTACA	ATAAGTCAGA	TGAAAAATAA	TAATAAGCTC
7701	CAAATTTTCT	ATAATGGACA	TATATATATA	TATCACTTTA	GTAAAGAGGG
7751	AAAATGCTTT	GGAATATATA	TGTTATATAT	GTATTGATAC	ATGTTAAACT
7801	TTTTATTTTG	AGAAAATTAT	AGATTTATAT	GCTAGAATAT	ATTTTGAAGT
7851	GAAAGTGCTT	TTGTAAAGCC	ATCTTTGGTA	TAAATTGCTG	CTTTGAACCA
7901	CCTCAATAAG	TGTGTGCCCC	TCAATCCCTC	TCTTCTAGAA	TAAATGGACA
7951	ACTAGTGGCT	TTAAAAGTCA	TCAGCATGAA	TGCAGAGGAA	GGAGTCCCAT
8001	TTACAGCTAT	CCGAGAAGGT	AAGAACAGCA	GAAATGGACC	CAATAGATCT
8051	GTGTTGAGTC	CTTGATTG	TAAAAAATGT	ATTGCATTGA	TCCATTGAGC
8101	ATCTAGTTTT	GATTCTTCTG	GAATACTATA	ATTACATTTT	TATTTTTCAT
8151	ACAAGTTTTT	CAAGAAATTT	ACACTGCTAT	TTTATTACTT	AATTTTGAGG
8201	AAATTGAGAT	TTAAAACAT	TATATCACTT	GACCAAACT	ATAAATTCAC

FIGURE 3C

8251	TGAGCAATTA	CTAATACTTT	CCATGTGTTT	GGCCTCATGC	TAGGTGCTAA
8301	GGCTATACCT	ATATAACCTC	AGAAAATTCC	TATAAAAGAG	AAAATATATA
8351	ATCACACAAA	TTCTTACTGG	GAAATTTGCC	TGAACATAAC	ATGTTGTTAG
8401	CTAGCACTTG	GAGATTCTCC	AGAAGGCATG	CATGTTTAGT	GTTACTGCCT
8451	GTATTTTCTC	TGTGCCCTGG	ACAGTACAGC	AAATGGGTGA	GGAACCTGGT
8501	GTCAAATGGA	CTTGGGTTTG	CAGCACAGGT	CCACCAATCA	CTAGTGGTAT
8551	GATGTTGGGT	AGGTTACTTT	AGCTATTTAT	TACTCAGTTT	CTTGCAGGAA
8601	GAGGATAATA	GTGGTACCTA	TTTCATGGAG	TTGTTATGAG	TATTCAACAA
8651	GAATATGTAT	ATAAAGCACT	TATCACAGAG	TCAGTTTTTC	AGAGTTCAAC
8701	AAATGTTGAC	CATTTTTATT	CCATTCTTCT	TTTCCTGGGT	AATGTCTTAT
8751	TTACCATCAA	GATAACTAAT	ACTTTATAAC	ATAAACATCA	AGAAGCCAAC
8801	ATAGTGAAAT	GAATCATTA	AAATATAATT	TATCAACCTT	TATTGCATGA
8851	GCCATTTGAA	ATAAGATGAT	GATAGGATTG	CTATGCATTT	CAGCAAAATC
8901	CCAGAGAAAT	GGCACTTCCC	TGGCCTTATT	TTCTCCCACT	TTTAACTACT
8951	TATCTTCTGT	TCTTTACTGA	GCACATGCTA	TATGCAGAGT	ATGCTGCTGG
9001	ATGCTGTGAA	GGATGAGAAG	AGAAACCCAT	GTCTTTGTTC	TATCATTTGC
9051	AGTCTTAACA	GAGCACATGA	TTCAAGTTAC	AAGTGTATAA	AAGACATAAA
9101	CTAAGATGAG	AGCAAGTTAG	TCTCAGTGTG	ACTGATGGAG	TCACTAGATT
9151	TTGAACTGAG	CTTGGAAGGA	TAGGTTATGC	AAACAAGCAT	GGAAAAAGCA
9201	ATTCAGAAAA	TGAGTTTATA	ACTGAATTTG	ATACCCTTTT	CAAAAGTCTT
9251	TCAGAGCCCC	TGAGGAATAC	ATCATTTTGA	ATTTAATTGG	AAGGGCCAAA
9301	TGGGCTATTG	GTTTAGCCAG	AGATTCATCC	TGGTAGGATC	AGGTGCATTC
9351	TGGGAGAAGG	CATGGTTTTA	AGTGTTTAAT	ATAATGGAAA	CTGCATTAA
9401	TAATGTACTT	ATTAATGGTC	TCCATGAAAG	GATGATCAGA	TTTGGAAAGA
9451	GATGTATGGA	TAGGTTAAAG	AGTATTTGTG	AACGTAATAG	AAATTCCCAG
9501	GTCACCCGCA	TAAGAGGAAG	GTTTCCTTTG	TGAGCTTGAG	TTTGCCAATT
9551	GCTTAAGATT	GGCTTTGCTT	AGATATTGCC	CACAGCCAAG	TTTTTCAGGT
9601	TGACATTTAA	CTGTAACAGT	GAAACCTTTT	GCCAGGTTTG	CTAACAGATG
9651	GTTCTCAGCA	TGGTTCAGAA	AACCTGGATC	CGTTTTCTTC	TGTATGCTAA
9701	ATGTTTCTTT	CATTGCATAT	TTACGGAGGA	ATTGCCTCTC	CATCAGAGT
9751	GTTTACAATT	ACATTTAGTA	GTCAACTGTG	GACTTTCTTG	GTTTGTTTTA
9801	TGGACTTACC	TTACCGAATG	CTTTGCTCGT	GTAATATTAA	AAACCACAAG
9851	AGGATTTCTG	ACACATTGGA	GGTTGTTAGG	AATCCAATTT	CCAACAATGA
9901	ATGTTTCTTT	TTACACCACT	ATAAAAGCTT	GGAGCCCTTG	TTAAAAGAGC
9951	CCTCTCCCCT	CAAGAAGATA	TGAGGCTTTA	TTCGAAAAC	TTGGCACTGT
10001	CCCATTTTTT	CTGTAAGAAC	TTTAAGGATG	TGAGACCAGG	GAGACAGGAG
10051	GTAAATGAG	AAGGGCTGGA	AGGCAAAGTA	AGAACAGCTG	GAGTTCATTA
10101	GCTAAAATCC	AGGGTCACTA	GCTAAAAGG	CAACCGAAAG	GCACGTGCAG
10151	GAAAACGAA	CAAGTAATGC	AGCCCTCTTT	AAAAAGCCTT	GAAGCAGGAA
10201	TTGCTTTTCC	TGAACAATTT	GGCTGCCCTG	ATGGTATAGC	AGCCAAAGAT
10251	TTATTAAGTA	TGATTTTACT	ACATATATGG	TCTCTTTCTA	TACAGGTAGA
10301	ATACATGTGG	CAATTTACTA	GTCTGGTCAT	TTGGAGTACT	ATTTTCATTT
10351	GACCTTAACA	TGTGATATTA	TGAAACTAGC	AAAAGTATGA	ACAGCACTAA
10401	GGAACATTTT	TTTTTTTTTT	TTTTGAGACG	AAGTTTTGCT	CTTGTTGCCC
10451	AGGCTGGAGT	GCAATGGCAC	AATCTTGGCT	TACTGCAACC	TCTGCCTTCG
10501	GGGTTCAAGC	AATTCTCCTG	CCTCAGCCTC	CGGAGTAGCT	GGGATTACAG
10551	GCATGTGCCA	CCACACCCAG	CTAATTTTGT	ATTTTTAGTA	GAGACAGGGT
10601	TTCCCCATGT	TGGCCAGGCT	GGTCTTGAAC	TCCTGACCTC	AAGTGATCTG
10651	CGTGTCTCAG	CCTCCCAAGG	GAAATATATC	TTAATACATG	TGTCAGTGCT
10701	TTTCATACTT	CTTTCAATCC	TCTTAACAAT	CTTTAGAGAT	AGATATTATT
10751	AATATTATTC	CACTATATGG	TGGTGATTCA	AACCAAATCT	CTCTGATTCA
10801	AAAATTTCATA	GGCTTTCTAC	GCACCCACTG	TAGAAATATT	CATTTAGCAC
10851	CTACTATGAC	CAGGTACTCT	GCCGAACCTG	TAGATACACA	GCAATACACA
10901	AAATAGATGT	GTTCCCTACC	ACCCCTATTG	CTTTGCTAAT	TAAGAAAAGC
10951	AGAGGCCTTC	ATAGTGCCTT	GGAAATCTCT	CATAATTGAC	TCTAGAATTG

FIGURE 3D

11001	TATTTTAAGT	GTTGATTTTT	ACAACTAGGA	GGAAATACTT	TCATTTGAAT
11051	AGGCTAATGT	GTTATGTTTT	TACATAGTAC	AACATTTCTT	AGTTTTATGA
11101	AACTTTATAG	CAATATCTTA	ATATAATGTG	CATTGTTTTA	AATATTTTTG
11151	TTCAAGTGGT	CAACTTTTGG	TTTAAACTGA	GGACTTTCAG	CCTGTTAATA
11201	GCATTTTTCT	TAGGAAGGAG	TCATATAACT	AATCTTTTTT	GAGGACAAGG
11251	CATATGACAT	AATCTCCCCC	TTCCCCTACA	TAATGTATAT	TTTTAAAACC
11301	TTTATACCAA	CCCTAGGAAG	TAAAATGTGC	TATTTTTGTT	GTAGAGATAA
11351	AGAAATTCTA	GCCTCAGAGA	GGTTAGTTAA	CTTGTCTGAG	GTCACAGAGA
11401	TAGTAATCAG	AGTTGTTAGA	ATCCATTTCT	ATTCTATTTA	AAATCCCTTC
11451	TACTTTATTA	TGATGAATTT	GGAAATGCTT	AACTAAAGTA	TTTATTGTTT
11501	AGCAACAGTA	AAAATAAAAA	TAGAAATCTG	TTTTTATTAT	ACATTTTATA
11551	TAAACGTTAA	GGAAAATGCA	GAAGAAGTAT	TTTTTTAATC	TTTAATTTTA
11601	GATTCAAGGG	GTACATGTCC	AGGTTTGTTA	CATGAGTATA	TTGCATGATG
11651	CTGAGGTATC	TTGTCAACCA	AATAGTGAGT	ATAGTACCTG	ATAGGTAGTT
11701	TTTCAACCCG	TGTCCTCTC	CCTTCCTCTC	CCCTTTTGGA	GTCCTGGTG
11751	TAGTGTCTAT	TATTCCCATC	TTATGTCTGT	GTGTTCCCAA	TACCCCCAGT
11801	TATTAGCTTT	CACTTGTAAG	TGAGAACATG	TGGTATTTGT	TTTCTGTTCC
11851	TGGGTAAATT	CACTTAGGAT	AATGGCCTCC	ATCTGCATCC	ATGTTGCTGC
11901	TAAGGAAATG	GTTTTTTTTT	TTCTTTTATT	TTGTGGCTGC	ATAGTGTTTT
11951	ATGGTGCCAG	TGTACAAATT	TTCTTTATCC	AATCCACCAT	TGCTGGGCAC
12001	CTAGGTTGAG	TCCATGTCTT	TGCTATTGTG	AATAGTGCTG	TGACGAACAT
12051	AAAAGTCTAG	GTGTCTTTTT	GACAGAACGA	TTTATTTTCC	TTTGGGTATA
12101	TACCCAGGAA	TGGAATTGCT	GGGTCAAATG	GTAATTCTGT	TTTTGGTTTT
12151	TTTGAGGCAG	GAGATGGGAC	TCGACTCCAG	AGATGGGGCT	TGAACACTAA
12201	ACCAAATTTA	GGACTAGCCA	AAACAGGGCC	TGGGGGGAGG	CAGCTTTCCA
12251	GAAGACACAC	CCACCAGTGT	GCCATGTCAG	TTTACCATTG	CCATGGCAAC
12301	ACCTGAAAGT	TACCACCCTT	TCCCGTAGCA	ACAACCTGAC	AACCTGGAAT
12351	TACCACTCTT	TTCTTAAAC	TTTCTGCATA	AACTGCCCTT	TAATTTGCAT
12401	ATAACTAAAA	GTGGGTATAA	ATATAACTGT	AGAGCTACCT	ATGAGCTGCT
12451	ACTCTGGGCA	CACTGCCTAT	GTGGCAGCCC	TGCTCTGCAA	GGAGAGGTAC
12501	ACCCGCTGCT	GCTGAACACT	GCTGCTTCAA	TAAAAGCTGC	TGTCTAACAC
12551	CACAGGCTCA	CCCTTGAATT	CTTTCCTGGG	TGAAGCCAAG	AACCTCCCCA
12601	GGCTAAGCCC	CAGTTTTGGG	ACTTGCCTGC	CCTGCCTCAC	TTTGAGAAAT
12651	TTCTAAACTG	TTTTCCACAG	TGGCTGAACT	AATTAACATT	CCCACCCACA
12701	GTGTATAAGC	ACTCCCTTTT	CTTCTCAAGC	TTACCAGCAT	CCATTAACCT
12751	TTTACTTCTA	AATAATAGCC	TTTTTGACTG	GTGTGAGATG	GTATCTCATT
12801	GAGGTTTTGA	TTTGCAATTC	TCTGATGATT	CGTGATGTTG	AGCAATTTTT
12851	TCATATGTTT	GTTGGCCACT	TGTGTGTCCA	AAAGAAATAT	TTTAAAGAAA
12901	ATAATACATC	ATGTTGTATA	TTTATCAATT	CTGATTCTAT	CATTGATTCT
12951	ACAGTGCCGG	TAATTGCAGT	GTTTAAATTA	GAAACAGTCT	CAGCTAAGAA
13001	TCTTTTAAGA	TCATTCTCTA	GTAGAAAAAC	ATTACAAAGT	AATGATTCCC
13051	AATCCATATA	TGAGAAAACT	GAGCCAAAAA	TAGGCTAAGG	AGCCTCCCTA
13101	AGGTCATACA	ATGAGGCAGG	GGAGGAGGCT	GATTAGAACT	TCTGAATTGC
13151	CAATGACCAC	AAATAGTCTA	GGGTAGGCCT	GGTTGACAGA	AAGTCTGCCA
13201	TTGAACACCA	TCATATCACA	TGACAAATAC	AGCAAATTCA	TTGTGCATAG
13251	TTACGTCTTT	ATAAAACAAA	ATAATGCCAG	GATAATGGTA	TGTGATCAGC
13301	ATTACAATTC	CAAAGATACC	AAGACAACCTA	CTTATCTGAC	ACTTGTCTTA
13351	GTATTTCTCT	AACATTTATC	TAAAATTATT	TCAATTATTT	CTTTTCTCGG
13401	AATGCATAAC	TTGACTCATT	GACTTGATTT	ATGATTCTCA	GATCAAAGGA
13451	AATGTAACAA	CAGGGACTAG	AAACACTTTT	TTATTCAATG	TCCAATGAGG
13501	GTTGGGGAGG	ACTCCATCAT	TGACTCATTA	TATAATTCTT	CATAAACTCA
13551	TTACAATTGG	CCTGGCTTTT	ATTAATTTCAT	GAGCACTTAT	TGAGCACCAC
13601	ATGCCAGGCC	TGTGCTAGTG	CTGGAGATGC	AAAGACAAGG	GCAAGTTCAA
13651	TCCATGCCCT	CAATGAGTTT	ACAGCCTAAA	GACGACTTTG	ACTACCAGGC
13701	CTTCATTACA	TAGAGCGACA	TCCTAGGACT	TGGAGAATCA	GCTTTCCTCT

FIGURE 3E

13751	GGAGCCTTAA	AGACATCCCT	ATTTACTTTT	GTGTCTTTTC	TTTGAAGAAA
13801	AACAAAAATA	AGTATACATA	GGATACATTA	ATAATAAAAA	AACAGTATTT
13851	TATGAGACTC	AGAATGCTAA	TTTTAGGATC	TTTGCCCTTC	TCAGTTGACT
13901	TTTGTGTCCC	TCAACTGTTT	AGTCTGCAGG	ACAGATATCA	CATCCTGCTG
13951	TGCAGTTTAT	AAAATGTCCT	TAAAATTAGA	AGAAAGAAAAG	GCCTTGTCTT
14001	CCTGGGTTTA	AGACCCACAC	ATCTGAGGCT	GTAGGCATTT	CAGATCCCTC
14051	TGGTGGATGG	ACCAAAATGA	TAAACAATAC	TGTGAGATAA	ATGCTTTAAA
14101	CATCATCTGC	TCTTTCATCT	GAATTCCCTA	TTCATTATTC	GGCAACATTC
14151	ACAGTTTTCA	TATAACGATT	TCAGTAGTTC	TAGGGCACCA	GAAAAGCAGT
14201	ACTAGGAATG	GCCATAAAGC	ATAGAATATT	TATAATCTAA	TGAGGGAGAC
14251	AACTAAAAGA	AAGAAGGAAT	AAAAGCATCT	TCAACAGAAA	CACCCTTTAC
14301	CAACCAACTA	GAGGTATAGA	AATGATATTA	GGTAATTAGT	GACCACTAAT
14351	TTAAAGATAA	ATATTTATTG	AGTGCCAGAC	ATTGTTCCAG	GCACTGAGTA
14401	TATAGCAATA	AGCAAAAAAA	ACAAAACAAA	ACAAAACAAA	AGTGCCCACT
14451	CTCAATGGAG	TTTATATTCT	CAATTGTGGA	GACAGACAAT	AAACAAATAT
14501	TTATATATAA	AATGTCAGAT	GGTGGTGACA	GGCACTATGG	AAAAGAATAA
14551	AGCAGGGCCC	AGAGAGAGAG	GGTAGGATGG	GGTAGAGGTG	GGATGGGGTG
14601	GAGGGCTGCT	GAGGTGGGAT	GGAGTAGAGG	GCTGCTATCT	CACCTAGAAT
14651	GGTCAAGGAA	GTCTGCACCT	ATATGTATCA	CTTGAGCGGA	GGCTCTGAAG
14701	AAAGTGAGGG	AGGATGAAGG	CAGAGAGGTG	AGAAGAGAGG	ATTACAGGAA
14751	AAGACATTGG	CAAGTGTAAG	ATCCTGGGGT	GGAAATGTGT	TTGCAAGTGT
14801	GTCTAAGGAA	CAGCTAGGAG	GCCAGTGAGG	CTAAAGCCAA	GTGAGCAAAG
14851	ATGGGAGTGT	GAGGAGATGA	CAGGTCACGA	TGGGCACAGC	CAACAGTAGG
14901	GTGGGCAGGA	AATCGCAAGT	CCTTTGAATT	TACTCTGCAG	GAGATGAGAG
14951	GCCACTGGAG	GGTTTGGAAC	CAGGAGGCAC	ATGCCCTAAC	TCATTTGAGA
15001	AGGATAGCAG	TGTCTGGCTG	TCCTGTGAAG	AAGTGGCCAT	AGGAGGAAAG
15051	CAGGGAAGCA	GGCATTTGCA	ATAATTCAGC	CAACATATGA	TAGTGGCTTG
15101	GTCCAGGGTG	CTGGCAGAAG	ATATGGCAAG	GGAGGGGTTC	TGGACAATTT
15151	GGAAGGTAAT	GCCAATAGAT	TTGTATGTGA	TAAAAAGTTG	AGAGGACTTG
15201	ACGTGTACGA	GTGGTTAATC	TTCATAAAAT	GGATGAATGG	TTAAAAAGAT
15251	TTCCGCAAAG	AAACTGTGGG	TTGAAGGTAA	AACATAGTAA	TCCAATGTAA
15301	GTGAACAACA	GAGAAATACA	AAACAGACAT	TTTTCTACT	CCTACAAAAA
15351	CTGTAATTAT	CAAGAAGACG	ACATGAAGTT	TATACCCAGT	ATTGTTAGCA
15401	GGAAGCCTCA	TTCCAAGTAG	ATATTTTTCC	TTGGCCATTT	TAGCAAGTGA
15451	GAGCATGAGG	CCATCATAAT	GAACAAATCA	TGCCATCATG	ATTTAAAAAG
15501	AAGCATCTGG	AGTTTTAGTA	ATATAGTTAG	GTGAGACTAA	AATTATACTA
15551	AACATAAAAT	TAAAAATATCT	TAACAATATT	CTTAGCAATT	TCAGCTTTAC
15601	CATATCCTTT	TGAAATCTAA	TTTTGCTATA	TGCTTTGTAA	CATAGGGGTG
15651	GGGGAAAGAG	AGAAATTTAT	GAGATAATTT	ATAAATAAAA	ATACACCTAA
15701	AGTATAAGCA	TTCTCAACTG	ATGGTCAGAA	AATATGGAAG	GTATTCAAAA
15751	CTCTAGCAGA	AACATACCAT	AAACAAGATT	TTAAGACTGA	AAGTAGACGT
15801	TTAGTGGGGT	TCAGGGTGAA	AGGCAGGGGC	AAGAAGCTGG	CAAGAAGAGG
15851	GAAGGGATAC	TAATTCTAAT	TTGCCTCTGT	AATGCTTTAC	ATTTACCAAG
15901	GTTCCACAAA	TGGTATCTGA	TTCCATCCTC	ATATCAACCC	TATGAAGTAA
15951	GTCAGAAAAG	ACGATGTCTC	TTTTCTAAG	GAATGAATTG	AGACTTAGGT
16001	TGAGATACTC	TCCAGAGCTT	ACTCAGATAG	GAAGTGACAG	GGCCAGGATT
16051	CATATTAGGG	CTTCTGGCTC	CACAGACAGT	TCTCCTTAAG	ACTTTCAATA
16101	AATATGTTTT	ACAAATTAAG	TGCTTACTCT	CGGCTGAGTG	TGGTACTAGG
16151	TGGTGTGGCA	GCATCTCAAA	AAGGGGGAAA	GTCACCTCCT	CAATTCCCAT
16201	GTGGCCTTCA	GTCTGAGACT	AGGGAGATTA	AACAGATGCC	TGAGAAGCTG
16251	TTTATTACAT	TTACAAAGCA	ACACATTTGT	CAAAGTGAAA	TAATAAATTT
16301	AGCCCAATAA	GACTCTGGGG	GCAAAAAGTA	AAAATTAAGG	CATTAGTCAT
16351	TACAGCAAAAT	AAGGTAAACA	GGTGTGATGG	AGCTCCTTCG	GCGTAAGTCA
16401	GCTTAAATTG	ACAAGTAAAG	AGAGAAATTC	ACTGGCTCAC	AGATCTGATA
16451	ACTACAGGCT	GGTAGGGCAT	AAGCAATATC	ATCAGGAAGC	CGTGTCTCTC

FIGURE 3F

16501	ATTACCCAAC	ACTGGTTTGC	TGTGCATTCA	TTTTATTCCC	AGGCATGTTG
16551	TCACCAGGTG	TTGGTAATCT	GACCCCAGCA	ACTCCTGGCT	AAATCCCACA
16601	GGTTTAGCTC	TCACAATAGA	AAAGAAAGCA	CTTCTTTTCT	AATGGCACCA
16651	GCAAAACAGG	GTCTGCCAAA	CTTGGGTTTT	GTGCCTGTCT	CTGAACCAAT
16701	CACTAGGGTA	TAGGGGAGTG	CCGTGCTCTG	ATGGCCAGCC	CTGGGTCATA
16751	TGCCCATTCT	TGGGTAGAGG	CCGGGTCAGT	TCCACCAGAT	GAGCATGGTC
16801	TGAGGAAGAA	GACGGTTGTT	TTTCCAGGGG	AAAATAGAAG	TGCCCCCGCT
16851	AGAAGGGAGA	ATGGCTGTCA	GGAGGGCAAA	ACGACAGATT	CACTAAAATA
16901	GGTTGATGCC	TAAAGAAAAT	AATTTTATTTC	CTAAATTTAA	GGGAGTATTT
16951	CAGTTGTTTT	TAATCTTATG	GAATTCTACA	CTGGGAGGGA	GTTGGTGCAG
17001	GAGATTCATG	ATATGCAGGC	ATAGGCTACA	GAATAATGCT	TTGAGTTTTT
17051	ATCCTTTACT	TTTCCTTTCC	TTTAAGCTTT	AAAGACACGA	TTTCTTCATG
17101	CAGGGTTGCC	CTGAGGTGAG	CCTCATCATC	TCTTTTTTTT	GAGATGGAGT
17151	CTCGCTCTGT	CACCCAGGCC	AGAGTGCACT	GGTGCAATCT	TGGCTCACTG
17201	CAACCTCCAC	CTCCCAGGTT	CAAGTGATTTC	TCTTGCCTCA	GCTTCCCGAG
17251	TGGCTGGGAT	TACAGGTGTG	CACCACCAGG	CCCCACCACG	CCCGGCTAAT
17301	TTTTGTATTT	TTAGTAGAGA	CGGGGTTTCA	CCGCGTTGGC	CAGGCTGGTC
17351	TCAAACCTCT	GACCTCAGGT	GATCCACCCA	CCTCGGCCTC	CCTGAGTGCT
17401	GGGATCACAA	GCATGCGCTA	CCACGCCCGG	CCTCATGGTC	TCTTTATTGT
17451	ACCTTTTCTA	GTCTCTGCTT	TCCTGAAGCC	AGAGGTCTTC	CTATCTCCAG
17501	AAGCTCCAAA	GACACACTTT	CAAACCCCTC	CCAGTCACTT	GGCCTTTTCT
17551	GATGACTTCT	TTCTTCAAG	GCTGCCTTTA	GTAACCGATT	ATTGAAGAGG
17601	CAAGAGAAAG	CCCTCAGCCT	TCTCCACTTT	CACCTCCCTG	GGCTCCCCAA
17651	GTTTGGCCGA	CTCCTCTTTT	CAAGTTCACA	TTTTCTCCTT	TCCACAGAGG
17701	TTTGCAACAT	TACCTTTAAG	AAATCATCTC	CAGTCTCTAT	CACGTTTCAA
17751	CAGTTCTTTA	CCCCATGCTT	TTATCCCTGT	CTCCCACCAA	TCATATCCAC
17801	CGGCCCTATT	GACCGCTTGT	GGGAGTTAGA	ATTTTGGAGA	CTGGTCATAT
17851	GTCACAAAGT	CCTGCTCTAG	AAGGCAGAAC	ACTCCATTTC	CTGCTCCTCC
17901	AAAGCCCTTT	ATCTCTCCAG	GCCTCTCCTC	CTGTAGCTCT	GAAGCTGGAT
17951	TGATGAGATT	CCCAGAGGGG	AGCATTTAGT	GCTCTGAGTG	CTTTGATGAA
18001	ATTGATTAGG	TAAATGGAAA	CATATTTTTT	GCAACCACTC	TAGCCTGTAG
18051	AAACAATAAG	TTGCAATGAT	TTGCCATTTT	TGAAATAATG	AAGGTTCTTT
18101	GTAATTTTAA	ATATTCTTTT	GCCACAAGAG	ATTGTTTTCC	AGCAGTAAAA
18151	TAACCAGAAT	GTTTGATTTG	AAATGTTGAA	AAAATATATA	CCGTCTGATA
18201	TCTTTAGAGC	AGCACTTTCA	TTATCAATGA	TGGATTTAAC	ATTTTGTTTA
18251	ATTTTTCTAG	CTTCTCTCCT	GAAGGGTTTG	AAACATGCCA	ATATTGTGCT
18301	CCTGCATGAC	ATAATCCACA	CCAAAGAGAC	ACTGACATTC	GTTTTTGAAT
18351	ACATGGTGAG	TTGTTGAGC	ATTTTACAAC	ACTTGAGAAA	AATAACCTGG
18401	TACTTGTATA	ATGAATCTGT	TAATATTTTA	TGGCATGATA	AAACTTTTAT
18451	TATAATGTGA	AAAGTATCAT	GGAAATTTTC	ATTATTGTGA	TTAGTAGAAC
18501	CTTATTGTTT	CCACATCCAT	CTTTGGTCCT	GCTTCCTTAC	CCATGACTTT
18551	TGCTGTCCCT	TTTCCCTCA	TCAGCAATAA	TAAATGAGGA	TCTTGAGTTT
18601	ACCTTCTAAA	TAAACTTTT	GCACTTATTT	TTAATCTAAT	TTTAATCACT
18651	ATCTGAGCAG	AATCCAACAT	TTTTTCATTG	ACAATAAAGG	TAAAAATCAC
18701	AAGATATTTA	AAAATTGTAT	GCAAGCTTGC	TAAAGAATAA	CTCATGTTGT
18751	ATTTTTGGAA	GAAAAAATAT	TTAAATAAGC	AGAAAGAACT	TATAAGGTAT
18801	GTGTACTTGA	CTTGCCTCCA	AGGACACTTG	GAGAGTGAAA	AATTCCTGCG
18851	TCGTTGTGTT	CAGTGCCAGT	CATTTAAAAT	GAGCATCTCT	GTGCTGAGAA
18901	ACAGGCTTTG	TTCTAAGAGC	AGCCAGTTAG	AAAGACACAC	TGTGTTTGAC
18951	CTTAACAGTG	GGTTCTCAGA	AAACCTGGTT	ATATTCCTTT	TGCACCTTAT
19001	TCTTAAAATT	CTGTACTTCG	TGATACCTTC	TGACAGTCAA	GTCAATGTTT
19051	TGCTTTAGGA	TGCTATCTAA	GCACCACTAA	ATTCACCTAC	TTCTCTTTCT
19101	CCGCTGTTTT	ATTTAGCACA	CAGACCTGGC	CCAGTATATG	TCTCAGCATC
19151	CAGGAGGGCT	TCATCCTCAT	AATGTCAGAG	TGAGTACGTT	AAGGGTCAGG
19201	ACCCTCTCCT	GGCTTGCCCA	CAGAAGGAGA	ATTCTGAAAC	AGACTGTCTC

FIGURE 3G

19251	ACAAAGCAAA	GTCCTATGAT	ACTAAATAAG	AGGATGGACA	TCCTGATAT
19301	TCCAGAAAAA	AGTTTTGTTT	TGTTTTTCGTT	TTTGTTTTTT	TTTAAAAAGG
19351	AAAGAAAAAA	GAAAAAGAGT	TGCTGAGTTG	CTTCTTAAGA	TATGGAGCAA
19401	TGTTTTCTGA	GCAACCTAAT	GCTGTCAGTC	ATGGCTACAT	GCAAATGTGC
19451	CTTTAGATGA	ATAAACGAGT	GAAGGAGAAT	TATACTAAAA	GGAAAAAAGT
19501	AAAGCTAGGC	CATCAAAAAA	TAAATAACCTT	CTTCATATCA	GATTACTGTG
19551	GTCTAAGGTG	AAGTCTGCAA	TACTTGTACT	AGCAGATCCT	ATTATATATG
19601	TGGCCCTAAC	TCCCATTTTT	CCAGTCATTA	GAATCAAAAT	AATAAACTCT
19651	TAATTAGCTA	TAATTCTACA	TCTGTTATAA	ATTTTAGAAA	CCATTTATAT
19701	TTCATACTTT	TCATTCCCTA	AGGTTTTATT	GGCATTAAAT	AATTGATTGG
19751	CTCTTAAAT	AACCGTATGA	AATTTGTATA	TGATGTATTT	ATTCATTTAA
19801	CTAATATTTA	TTTATGTATT	CATTTATTCA	TTCATTTAAG	AAATATTTAT
19851	TGAGTACTTA	TTGCGTAATA	AGTTCTGGGG	TTTCAATAAT	GAATAAGTTC
19901	TGTTTCTTAT	TTTCAATGAG	CTTAAAGTCC	AGTAAGATAT	ATGAACTTAA
19951	ATAGGCAGTG	AGGGCCAGTC	TTCAAGCAAC	AGCAATGCAA	GATGGCAGCC
20001	ACCATGGGCT	CAGGCAATTT	ATGAAAGCCA	AATATACAGC	CTTAAAATAG
20051	AATGTGGACC	TAAATACCCA	GAAGAACTCC	CCTTTGTAAG	ATTTGTAACA
20101	AAAATTAATA	TGAGTAGAGT	TAATAGTTCT	AATGGAATGG	TGAACCCAAG
20151	AGCCATATCA	GCGCTAGCAA	AATGGCAGAA	TTCATATATC	ATCAAACTTA
20201	TCCTTCAAGA	GCTTCAGCGC	CTAATGATGT	CTAAAGAAAA	TGTGAAACGC
20251	CCTCAGCCAT	CTGAAGGACA	GTGTTACAGC	AATTGATCAA	AAAGAAAAAC
20301	CACAGGCCCT	TCCCCTTCCC	CCATACTTGA	TGTAAGCAGT	CTTCATTTTC
20351	CATAGTAGTA	AATTTTCTAG	ATACAGCTTG	TAGAGCTCAA	AGTACTGGAA
20401	AGAAAGCTCC	CATTCAAAGG	AAATTTATCT	TAAGATACTG	TAAATGATAC
20451	TAATTTTTGT	ACATTTGGAA	TATATAAGTT	GTTAGCCTGG	CGCGGTGGCT
20501	CACGCCTGTA	ATCCCAGCCC	TTTGGGAGGC	CAGAGTGGGC	AGATCATGAG
20551	GTCAGGAGTT	TGAGACCAGC	CTAGCCAACA	TGGTGAAACC	CCGTCTCTAC
20601	TAAAGATACA	AAAAATTAGC	CAGGTGTGGT	GGCGCACACC	TGTAACCCCA
20651	GCTGCTCGAG	AGAGTGAGGC	AGGAGAATTG	CTTGAACCCA	GGAGGCAGAG
20701	GTGCAGCGAG	CAAAGATCAC	ACCAATGCAC	TGTAGCCTGG	ATGACAGGGC
20751	AAGACTCCAA	CTCAAAAAAA	AAAAAATAAT	AGAAATATGT	AAGTTGTGCT
20801	ATAACAAATA	AATAGGCAGT	GAGAAGCAAA	GTGCTAAAGC	CTATGACCAT
20851	GGTAACTAGG	AATACTGTGG	GAACACATAA	TAAGGGAACC	TAACCCAGTC
20901	CTGGAAGTAA	GGTTTTGGAA	AGGAATGTTT	GAGGACAAAG	GGTTAAAGAG
20951	AGTGAAAAAA	AAAATTAATA	TACCAGTTTA	GCTGTGTGGA	GAATGGGATA
21001	GGGAGCTAAC	TAGAGAAATC	AAATAGGAAT	GTTTCATGGT	ATGTTAAGGA
21051	CCCTGGTAAG	GGTGAAGACC	ATTACATTAT	CTGCACCATC	GCGGGACTTT
21101	TTTTTTATGG	TAATGCTTGG	CAATTTAAAT	AGAGGAGCAG	AGAATGTAGA
21151	CAGTTGGATT	GAGTCAGAGT	TGAAGTTCTG	CCAGACATGT	GAAAGGAAGA
21201	GACAGGTAGG	CAAGAGAGTT	GAAGAGATTA	TCAAGACAGA	AGTTAATGTG
21251	CTGGCCAGTG	GCATCTAGTC	TGAGTCTAAT	CTGAGGGAAG	GAAGTGAAGA
21301	TAAGCAGCTT	GCTGATAGTT	ATGAAGAGAG	TGGAAGGCTT	CAAGGACCTA
21351	CAGGTGTTGA	TTAAATAGAA	GAATGATTGG	AGAAAGAATA	ACTGTGAGAG
21401	AGTGAGATTT	TCAGGCTTGA	GTGACTCTCA	CATACCAGAC	ACTGTGCTAA
21451	ATGCTTCAAA	GACATGATCC	CTGCCCTCAA	GGGACTTACA	GCCAAAAACA
21501	AGAGATAAGA	AATACACACC	AATACTATTA	TAGGACACTT	GTGTAGAATA
21551	TCAAGAAAGA	AATACGATCT	AGTACTGTAG	ATGTGCAACG	GCATCAAAGA
21601	TATCTTCTAG	TTTCAAGAAG	TTTCAGATCG	GCCGGGCGCG	GTGGCTCACG
21651	CCTGTAATCC	CAGCACTTTG	GGAGGCCGAG	GCGGGTGGAT	CACAAGGTCA
21701	GGAGATCAAG	ACCATCCTGG	TTAACACGGT	GAAACCCCGT	CTCTACAAAA
21751	AATATAAAAA	ATTAGCCAGG	CGTGGTGGCG	GGCGCCTGTA	GTCCCAGCTA
21801	CTCAGGAGGC	TGAGGCAGGA	GAATGGCGTG	AACCCGGGAG	GTAGAGTTTG
21851	CGTGAGCCGA	GATCGCGCCA	CTGCGCTCCA	GCCTGGGCGA	CAGAGTGAGA
21901	CTGCGTCTCA	AAAAAAAAAA	AAAAAAAAAA	AAAGTTTCAG	ATCTTAAACA
21951	CACTGCATTT	CAACAGTCTA	GAATAGGAGA	GCATGTTACA	GGGAGAGAAA

FIGURE 3H

22001	ATGTTTTTCAG	CAAAGGTACA	GAGTAGGGAA	ATAGAGGATA	TGTTCAAGGA
22051	AGAGGACCCC	AGAGTCATGG	TTTGTTAGGG	TTAGAGGAAA	CACAGTGTTC
22101	TGCAATCTCC	AGGTTCCATT	AGTGCGTTAT	GAAATCAATA	TGGTGGTTAG
22151	CAACCTGCAT	TTTAAAAAAT	GAAATAAATG	GATGAGAAGA	GAATAGAAAA
22201	TATTAGCATG	CATTACATTT	TGAAAGAGCA	AGTATTATTT	TCTGCAACTT
22251	TTGCTCCAAT	TGTAAGTGA	CTTATATTTT	TATGTATGGA	TGTGAATACC
22301	AGATACATAT	ATATTTCTTA	CTGTAGACTG	CAGTCAAAAA	ATCTTTAAAG
22351	CACTGGCCTG	GTCTAACTTC	CTTATTTTGC	AGAGGAGAAA	TCCAAGATCT
22401	GAGAGGACAA	ACATTTTGCC	TGAGGTTATA	GAACCAGCTT	ATGCCATTGC
22451	TAAAAGTGAT	TCTTAGTTAA	AATTCTTTCC	CACTAGTGCC	ATACTGCACT
22501	TCTAGTTCTG	TTGGCCTGAA	ATACAGAATA	TATTAGTGAA	ACAGCATACA
22551	CAAGTCTGGG	GAAATATATT	GGGTAGGTGG	CTGAGAGCCT	CATTTTCTAA
22601	GAAATGTGGA	CCTTAGGCAG	GGTATGGTGG	CTCACACCTA	TAATTCCAGC
22651	ACTTTGGGAG	GCCAAGTCAA	GAAGATCGCT	TGAACCCAAG	AGTTCAAGAC
22701	TAGCATGGGC	AACATAGCAA	GACCTCATCT	CTACAAAAAA	TTTAAAAATC
22751	AGCTGAGCAT	GGTGGCATAC	GCCTGTAGTC	CCACCTACCT	GGGAAGCTAG
22801	GTGGGTGGAT	CGCTTGACAC	AGGAGTTTGA	GGCTAAGGTG	AGCCATGATC
22851	ACACAAGTGC	ACTCCAGCTT	GAGTGACAGA	GGAAGACCCT	GTCCCTAAAA
22901	AAGAAAGAAA	TGTGGATTTT	ATTCTTTAGA	CAGTACAGTC	ATTAGTCATT
22951	AAGTTTGAGT	TGAGAGAAAA	TAATATGATC	AGAAGAAATT	TATATCACTG
23001	TGGTCTGTAG	GATATATGAA	AGGAAATAAG	AGACTAGAGT	CAGGGATTCC
23051	ACTTAAGTGT	TTGTTTGTTT	GTTTTGAGAC	AGAGTCTCTT	TTTGTTACCC
23101	AGGCTAGAGT	GCAATGGTGC	AGTCATGGCT	CACCGCAGCC	TCAAACCTCC
23151	AGCCTCAAAT	TATCTTCCCA	GCTCGGCCTC	CCAAAGTGCT	GGAATTACAG
23201	GTGTGAGCCA	AAGGGTTTAT	TGATGTGGTC	TGGCCTAGTG	CCTCTCAAAC
23251	TTCAAGTGAGC	AGACAAGTGA	CCGGGAACCT	GAAGTCAACAA	GTCTGGGTTT
23301	AAGCCTGAGC	CTCTGCATTG	TAACATGAGT	CAAGCTGATG	CAGATGGTGC
23351	TGGTCAAGAG	CCAAGCACTG	AGCAGCAAGG	ATCTAGTTAG	CAATTAGTAA
23401	TCAAGGTTGA	TATTATGGTA	GTGACAATAA	GAATGGAGAG	GAATGTGAAA
23451	ATCAGTAACA	AAGAAGAGTT	CACCTCTTGG	TAATGTGAGC	ATGAGAGGGG
23501	AAAGGATGGG	GCCAAACATA	ACTGTTTTTG	TGTTTGACTG	ACGAGGAGAA
23551	TTGTAGCTCT	ATTAACAGAA	ATAGGAGAAG	AAGTTGGTTT	GGAGAGAAAG
23601	AGGAGTCCTG	TTTCAGACGT	GTTGAGGTCC	CAGGTGAGAC	AGGATCTCCA
23651	AAGGGAAATG	AGCAGTAGGC	AACCTAAAAG	GAAATCTGTG	CTCAGAAGGG
23701	AGCTGTGAGC	TCGACGTGTA	GATCTGAGGG	TCATCAGCAC	ATAGAGTTTA
23751	GAAGACAAGG	AGTAGGCAAC	CAAAAGAGCA	AATACACAAA	GAGAGGAGGA
23801	CTGATGATGA	GACTTTTGCC	TTTTAGGATG	AGAAGAGGAA	CAGGAAATGA
23851	AGGAATGAAG	GGAAGCAGCT	TGTAGGAATG	TAGAGCATCT	GAAAAAATAA
23901	TACACACTGT	CATGGAAGTC	AAGGGAAGAA	GAATTTCAAG	AAGGAGGGTA
23951	TGGTGGACAG	TATTACAAGC	ATCAGGAATA	CAGCTAAAAG	TCATACTCTT
24001	GACTGCATTG	ACCTTGTTGA	TTTGTGAGGG	ACACACTAAT	AAATAAAGGA
24051	ATTTATTGTG	GGTATATGGA	GGCACAAAGG	AAGAGGTTAT	CCAAATCAAA
24101	GCAGGTGGGA	GTAGGGATGA	GTTCTCCAAG	GTGGAGGCAT	CAGTGAATGT
24151	GGGAAGGGGC	ACAGAGCATC	CATGCCCATC	CCAGGCAAGC	CACCCTCCAG
24201	AAGCCTCCAT	GAGAGTTCAG	CTATCCAGAA	GGTCTCTGTA	CCCTAATCTT
24251	TCTGGGTTTT	GCATAGGCTT	CATTGTGTAG	GCATGATTTA	TTAAACTATT
24301	GGCCACTGGT	GATCAACTTA	ACCTTCAACC	CCTCTCCCCT	CCCTAATCAT
24351	GCCTTGGTCT	TTCCAGTGAC	CAGTCCCTAT	CCTAAGCTAC	CCAATGGTCT
24401	GCCAGCTATC	AGTCAACTCT	ACAAAAAGAC	ATCACTTTGG	AGATTCTAAG
24451	GATTTTAGGA	GTTGGCTGTC	AGGAATTTAG	TTGAAGATCA	AATATATATT
24501	TCACAATATC	ACAGTCGTGC	TATTTTATAT	CAGGCGCCAT	TAAATGGTTT
24551	TAAACAAAGA	GGTGATAAAT	TCAGATTTTC	TTTTTATAAA	GCTTACACTG
24601	ATGACATGTG	GGTGAATAGA	TTGGGATGAG	GGCAATACTT	TTTTTTTGAA
24651	ATGTTATATT	CCCCTGACCC	TACTTTCTCC	TTGTTTTCTT	CTACCTCTCT
24701	CCCCCTACTC	ACACAGAAAA	CTTCTCTCCC	TCTACTCATT	CCCTGAATGC

FIGURE 3I

24751	TGGTGTCTGT	TAAGGTTCCA	GCCTTGACAG	TGAGGCTAAT	CAGAACCACA
24801	GTGGTACAGA	TGTGAGATGA	TGGTGGGAGA	AAGTGGACAG	ATATGAGACC
24851	AATTACTTAG	CCGGAACCTGA	CGGGAAAAAC	AAGAGTCAGC	GATATTTTTT
24901	TCTGGATCTG	AGTATTAAAA	TGGATGATGG	TGCCATTAC	TGTGATAGAG
24951	AATCAGAAAG	AAAAATTTAT	TTTGGAGAGA	TACCATGAAT	TGTGTTTTAG
25001	ACATGCTAAG	TTTGAGGTGA	TTATGGGATG	TACAGGCGAG	CTCCAGACTG
25051	TGTGGGCCCTA	AAGTAGAAAG	GCAATCTGAG	TTGGAGATAA	AGATTTTGAA
25101	ATCATCAGAA	TACGGTTGTT	CATTAGAGCA	CTGTCAGTGG	GTAAGATAGC
25151	TAAGGGAGCA	TGTGTAGAGT	GATAACAGAA	GATCAAAGAC	GGAACCCTAA
25201	GAATAACAAT	ATGTTATTAT	TTATTATTTT	ATTATGTTTT	ATTTTTTAAT
25251	TTTATTTTAA	TTTATTTATT	TATTTTATGA	CGGGAGTCTC	GCTCTGCTGC
25301	CCAGGCTGGA	GTGCAGTGGC	GCAAACCTCAG	CTCACTGCAA	CCTCCGCTTC
25351	CTGGGTTCAA	GGGAGCCTCC	TGCCTCAGCC	TCTCAAGTAG	CTGGGACTAC
25401	AGGCACCCAC	CACCTCACCT	GACTAATTTT	TGTATTTTTA	GTAGAGACGG
25451	GGTTTCACCA	TGTTGGCCAG	GCTGGTCTTG	AACTTCTGAC	CTTGAGTGAT
25501	TCACCTGCCT	TGGCCTTCCA	AAGTGCTGGG	ATTACAGGTA	TGAGCCACTG
25551	TGCCTGGCCT	ATTTTTGTTT	TTTATAGAGA	TGGGGTCTTG	CTATGTTGCC
25601	CAGGCTGGTC	TCGAACTCCT	GGACTCAAGC	AATCCTCCTG	CCTTGGCCTC
25651	TCAAAGTTCT	GGGATTACAC	ATGTGAGTCC	CTGCGCCTGG	CCAGAATATC
25701	AATATATTAG	ATTTTAGTAG	AAGTAGAACC	TATGAAAAGA	ACAGCCAGAG
25751	GGGCAGAAGA	AAAATTAGGA	GATTGTGGAA	CCAAAAGAAG	AGAGTGCCTC
25801	AGGAAGGAAG	GCATGGTCTA	TGATGCCAAA	TGCTGCAAAG	ATAAGGAATA
25851	AGAAGTATCC	ATTGGGTTTC	ATAGGAAAAG	TCATGGGAAA	CCATGGTAAA
25901	AAAACATTGT	GAATGACACA	ATCGTTGCAA	AAGCATTTTT	ATAGGGGGAT
25951	GAATTTTGTA	TTTCAGAGGA	CAAACAGTTC	CATACAATGG	CAAGATCTAG
26001	TGTGTGACCA	CGGGAGTTAG	TGTCTGAAGT	GGATTGGAGA	AGCAGATCAT
26051	TGGAGCTGAG	GTTGGCTAGA	GCTGTTCTCA	TGGACACTAA	TGTCATGGAG
26101	TCAACAGCTG	TGATCCAAGT	GCCACATCT	TCAGTGAATG	ACAGAGAGGG
26151	ATTGAGAGTT	CAGTGAATGA	CCGCTAAAAG	AAGAGTAATG	GAAGATGTGG
26201	CTGGATGGCA	TTAAAATCCA	AGGGACAGGG	GTTTTTACTT	AAAATAGAG
26251	AAGTAATGGT	TTTGAAGTGG	TAGTGGGGAA	AAGGGAGGCA	GCTTATGACA
26301	CTTGTCAGTG	GTCAAAGGTA	TGAGGAAGTT	ATAGAAAAAC	TAACATCCAC
26351	TTGAGAATAT	TATAGGGAAG	CAGTGAGCTC	AAGGTCTCAT	TTAAGGAAAG
26401	GAGCCAAAAG	GAAATTCACC	AGAGGTTAGC	TTTTAGGTAG	TTTTTAAAGC
26451	AGGATTGAAG	AATGGAGACT	AAACAGTGAA	AATGTTTGGG	AGAGAGAGGA
26501	GCAATAGATA	TGAGGCTAAA	CAGAGGAAGC	ACAGAACAGA	ATGGAGATGA
26551	GTATGTTGGG	AGGAAAAGGA	ATAGTCAGAG	GCTTATATTT	TGAGTTGTGA
26601	CCAAGGAAGA	CAGGGTGGA	ATCCTCGTGA	GGTTATCTTG	TTTCAGATTT
26651	CTAGTAGAAT	GAGTCCCAGG	GATTCCAGGG	GGGATGGAAG	GACTCAGGCT
26701	TCCCTATAAG	GAGTTGGCTA	ACGGATCTCA	TTGGTTTTTG	AGTAACTCCT
26751	GGCCCAGATG	GCACTAGTTC	AATGGAATTA	TTTTGTTCCC	CCAAAACCTA
26801	TTGAGTTGGA	AACAGGTCTA	ACTCCTGGGA	TCTGGGAAGC	CTTTCTGGAA
26851	AGAGTCACCC	ACGATCTGGC	TGATGTTGAA	CTGTGCAGAC	ACCATCATAT
26901	TTGGTTATGT	TAGGATGCAA	TAATTGGTGA	AGCTTCTGTA	GTGTTGAATG
26951	AAGAATCCAG	GTTGGAAGGG	ATGAAAGGGT	GAGTGGGTGA	TGAGGTTTGT
27001	CAGCACAGAC	TGCAATTTTG	AGAAATGTGG	TTATAAAATA	CCATACCTTA
27051	ATACCGCAGT	GCTTTACCAC	TCACAAATGC	CTGTAGACGT	ATCTGGCAGA
27101	GAGGAAAAGG	GTTGAATGGC	AAGAATGTGG	GAAGGGACTG	TGGCTAGTTA
27151	GTGAAAATAG	TCTACACTTG	GGACATAAAA	GGCATTTCAA	GCTGACCTAC
27201	TAAGAAGCTC	TGTCTCTGAC	TCAGCCAGCT	GGCTCTCTCC	TTCCCTGTCA
27251	TGTTTTTATT	TTCTGTCTTT	TCTCTAGTTT	CTCAGGATGG	TATAGTGGAG
27301	TCAGACAAGT	CTGAATTTGA	GTCTTGGCTC	TGACTATTCC	TAGACATGTT
27351	TTAAAAGTTA	CATTGAGCCC	TGGTTTTCTC	TGTAAACTGA	GGATAAGCAT
27401	GCTATCCCAA	AGTTTGTATC	CCTCACTGGT	CACCAGCTTC	CTGTCTTCTA
27451	TCCACCTGTC	TTCCTCTTCC	TCTTCCCTA	GTCCTGCATA	TTGAAAAACA

FIGURE 3J

27501	TTTTTTTTTT	TTTTTGAGAT	GGAGTCTTGC	TCTGCCACCC	AGGCTGGAGT
27551	GCAGAGGCAC	GATCCTGGCT	CACTGCAACC	TCTGCCTTCC	AGGTTCAAGC
27601	AATTCTCCTG	CCTCAGCCTC	CCGAGTAGCT	GGGATTATAA	GCATATACCA
27651	CCACATCTGG	CTAATTTTTG	TATTTTTAGT	AGAGATGGAG	TTTCACCACA
27701	TTGGCCAGGC	TGGTCTCGAA	CTCCTGACCT	CAGGTGATCG	GCTCGCTTTG
27751	GCCTTCCAAA	GTGCTGGGAT	TATAGGCGTG	GGCCACTGCG	CCAGTCTGAA
27801	AAACGTATTT	TTAAGCATAT	ACTATCGTAT	CTTCTTGTCT	TTTACCTGGA
27851	ATTTAAGCTG	GTTGTTTGTA	TTACCTTTTC	CATGGACATT	TATATTTATA
27901	ACCAATCAGA	AGGTTTAAAT	GTCAGTGTAG	GAATTTTGTG	CTATGGAAGC
27951	TTCGTGGCTT	GGTGAATGGT	AAAATGAATA	ATGTGTGTAT	ATTTGAAGCA
28001	TCAGAAAGAG	AAAATGCTGG	GAAGATTCAT	AGAACCAGTT	AACATTTGAA
28051	CTAGGAGTCA	TAAGAAATTT	TTAAAATTCT	TAAATGGTTT	ATGAACCTGA
28101	TGTGGTAGCT	ACATGAAACC	TGCATAGCTG	CAGGTATGCT	ATGGTAGGTA
28151	AACTCTCCAT	GCTCCTGCTT	CCATTGGACC	ATTTGGCTCC	AATGTCTCCA
28201	GGTCTTTGTT	AGATCAATAC	TGGTCCTAGC	ATCTCTGAAA	GTCCTAGCTT
28251	TCTAAGATGC	TGTTGAAAAA	GAGGATTAAT	CCACATAACT	CTGCATCTGC
28301	CATTTTGCCC	ATGTCCCAGG	AATGCTGGGC	CTAGCCCTTC	CTTTCTGAAC
28351	GTCCAGAACA	CGTTCTCAGT	TGACATACGT	CTTTGTAAAT	ACTGATGTTG
28401	GTGTTTGAAT	TCTCAATTGC	CAATGGCACT	GGAAAATAGC	AAAAGATACT
28451	TGGAATACTA	AGCATTCTTT	TTTTCCCGTA	AGTTTCTGTA	GTGATGGGAA
28501	CCTAGTAATG	GCTTTGGTTT	CTGTGCCTCA	TAACCACATG	AAACATTTTT
28551	AATTTGGGGC	TCAGAATGTG	TTTTTCCTT	TTATTTCTCC	ACCACTACCA
28601	TTTACCCTTT	CTCCCTTCTT	CCTCCTACAA	TTTGTTCTCT	ATTCTTTTTT
28651	GATTTTTTTT	GAGGGGGGGG	GGTCTAACTT	ATTTTGGTCT	CTCTTCCCTT
28701	TTCATCTGTA	CTGTGTATTT	CCCTTGTTTT	CAACTTTGAA	TTTAAGACTT
28751	TAAAAATAGC	TTTAAAAAGA	TAAAGATTTT	TTTATTTTCT	AATACCATCT
28801	AAAGATATAT	TTTTTAGTGT	GGTCTCCTTG	TGTTGTGTTT	TTAAAAGGGT
28851	TTCATATTGG	AGAGCCTGGA	AAACTTAAGC	AGTTGTAAAC	TTTAGAATAT
28901	CATTTCCAGG	TCAACTTTGA	TCTTATATGC	CAAGTTCATC	GGTGGGGAAA
28951	AAAATTAAT	CTTTACATAT	TAAATCAATA	ACTAGTGTTT	CAAAGGAAAC
29001	TTCAAAGTTT	CACTTTAGAT	TTTTAAAGAA	GGGTAATTCC	TTCCAGTATCA
29051	AAGAAATGAG	ATGTCAGGAA	AAGCCAGAAT	CCCTTTGTTT	AGGACACAGT
29101	CTAGTTACTT	GACTTTTCTT	GTCCTTTTTT	TTCCCCCTCT	GAATGTAAAA
29151	ATCTTCTTCT	TCTTCTTTTT	TTTTTTTTTT	TTGGTCTCTC	AAGAGACACT
29201	TTTACTATAT	TCTTTGAGAT	GACTGTTTTT	GATTTAGAGG	CGAAATCAGC
29251	ACGTGGTGGC	TCAAATCTCC	TTATGGATAG	TGTTTCTTCC	TTCCAGCTTT
29301	TCATGTTTCA	ACTTTTGCGG	GGCCTGGCGT	ACATCCACCA	CCAACACGTT
29351	CTTCACAGGG	ACCTGAAACC	TCAGAACTTA	CTCATCAGTC	ACCTGGGAGA
29401	GCTCAAACCTG	GCTGATTTTG	GTAAGTCGCC	CCTCGGGTCT	CATTCTGGGC
29451	TGTGAACAAT	GATGCTTTTG	TGTGCACTTG	TTTAAGCGTT	GACTGGGCCT
29501	GGCCTTTGAA	AACTGGAGGC	CCAAGAACAT	GATGCTTTGT	GAGGATATCA
29551	AATACCACA	AAGGAAGTGT	GAGGCACGAA	ACAGGGAGGG	ATTGGTAGCT
29601	TTCTAGGATT	CCACCAAGTC	CCAGTTTAGT	CAGATGGCCA	AAAGCTGGGC
29651	ACCCTTGCTG	CCCCACTGCC	AGTTTTGATA	TAGAGACATT	GGTAGAGTAA
29701	ACTGTACTTA	GTAAGTTTTT	CTAAATCTAA	GTGAATATAC	AAATTATATT
29751	GGAATAGATT	GAGATTATCC	CAAGATGATA	AAGAGGTTAA	CCCCAGATTG
29801	TAGCATGGAC	TCCTGTCAGG	ATGGAGACTC	CAGGACACTT	GTTCTGTCTC
29851	TCCTACCTTC	TTTATATAAG	TGTGAGATGC	AAAGTTTTAT	TCCCATTAAA
29901	GTGAAGCAGA	TTTCCTCTAA	GTATCACTGT	ATCCTTCCAT	TTTAGCACTT
29951	ATCGCAGTTT	ATAATTATAT	TCACACACAT	AAATACATAC	ATGCATACAT
30001	ACAAATATAT	ATACATGTGT	GAGCACACCC	CCACACACAA	ATATATATAG
30051	ATTTGCGTGA	TGATTTTGTC	TCAACTGGAC	TGTAAGCATA	ATGAGGGCAG
30101	CCTGGGTTTG	TTTTTGCTTA	TCATTTTATC	CTTAGTGCCT	GGTACCATAG
30151	TAGGTGCTTA	ATAAGTACTT	GTTGAAAAAC	TGGCTCTATG	TGAGCTAAGG
30201	AACCACTCTT	CTCTGTTTGG	CAGATGCCAA	ATGGTGATAC	TATCACTGCA

FIGURE 3K

30251	GTATTTATTC	TGAGATGGCA	GCTTTTATCC	TGACATGTAA	GCATTTAACA
30301	GATATTTGTT	TATCAATTCT	CCACAATAGC	AAACTCATCT	ATTGAAGTTT
30351	TTCCCAACAA	TAGATCATGC	AATTCTGTGA	GATAAACAGC	TGACTGACAG
30401	AAAGACTCAT	TTTGCAGAAC	AGTACTTAGA	AATTCATCTA	AGGTCCTACC
30451	AAACTAATTA	ATTTGGATGA	GCAGTCCCTA	CCGTTTATCT	ACTAAACTGG
30501	GCTTTCCTGG	AGTGCCAAAA	CGGAAGGTGG	CCATGTTAGT	CATGAACAGC
30551	TCAGTTTCTG	TTACAGAGAC	CCAAAATTAC	AGAGGTATAA	CATGCTAGAA
30601	ACTTAACTTT	CTTTCGCATC	ACAGTCCTGA	CCTAAGCAGG	CAGAGCATGT
30651	ATGGTGGCCC	CATGCTATCT	TGGCCCAGGC	TGCTTCTGTC	ACGTGGCTCC
30701	TCCATCCCCA	ATTGTATGTT	TCAAGATGGC	TGCCACTTCC	TGCTCATCAC
30751	AGCCCAGAGG	AGGGAGAAAA	GAGAAGCAGA	ACCCTTAACC	CCTCCACTAA
30801	GGCATAATCT	GGAAGTTCAC	ACATCACCTC	TGTTTCATATC	ATATAGGCAA
30851	GAACCTAGTC	ACCTGACCAC	ACCCAGCTGC	CAAGAAGGCC	ACATCTAGCT
30901	GCAAAGCAGG	CCAAAATTTG	AGAAATTCAC	TTGATGAAGT	GATAGACAAG
30951	AGTCAAGATA	GTGATTAGTT	CTACTAAAAG	CACCTAAAGT	TTGTGTGTTA
31001	TTTTTTCTAA	TGGTGTTTAC	CCTGGTCCAG	TGCATCATGG	TGCAAGCCAA
31051	GGTCCAGAAC	GATGGGTTTT	ATGCTTTTCC	CTTTTGGACA	GGTCTTGCCC
31101	GGGCCAAGTC	CATTCCCAGC	CAGACATACT	CTTCAGAAGT	CGTGACCCCTC
31151	TGGTACCGGC	CCCCTGATGC	TTTGCTGGGA	GCCACTGAAT	ATTCTCTCTGA
31201	GCTGGACATA	TGGTAAGAGT	GGTGCCGAGA	AAATGTGAGT	CATCCTACTC
31251	ACGAGGGTTG	CTTTATCATC	TACATTATAT	TTTAATAATA	ATTCTAAAAA
31301	TGGCAATCAC	GTATATATTT	TTATATATAT	TTATATTTAT	ATATTTTATA
31351	TATATTTATA	TAGTTATATA	TTTATATTTT	ATATATTTAT	ATATTTTATAT
31401	ATATTTGTAT	ATATTTTATAT	ATTTATATAT	TTTTATATAT	TTATTATATT
31451	TATATTTTATA	TATTTTATATA	TATTTATATA	TATTTTATAT	ATATTTTATAT
31501	ATATATTATA	TATATTTATA	TTTATATATA	TTTATATATT	TATATATATT
31551	TATATATTTA	TATATATTAT	ATATTTTATA	TATTTATATA	TTATATATAT
31601	TTTATATATT	TATATATTTA	TATATTATAT	ATATTTTTTT	ATATATATAT
31651	ATATGTATTT	TTTTTTTTTG	AGATGGAGTC	TCACTCTATT	GCCCAGGCTG
31701	GAGTGCAGTG	GCCAGATCTC	AGCTCACTGC	AACCTCCACC	TCCCAGATTC
31751	AAGCAATTCT	CCTGCCTCAG	CCTTCTGAGT	AGCTCTACTA	AAAAAATACT
31801	AATATTTGTA	GAAGATTCTT	GCAATTATTC	TATAACCTTT	TACTGTTGAA
31851	CTGAGACCCA	CAGAGTTCCT	GCCCAAGGCA	TCTTCTGAAT	CTGACACTCT
31901	TTTTATGTTA	TTTTATTTTT	TGAGATTGGG	GTCTTGCTAT	ATTGTCCAGG
31951	CTGGTCTTGA	GCTCCCAGGC	TGAAGCAGTT	CTCCCCTTC	AGCCTCTTGA
32001	GTAGCTGGGA	CTATAGGGCT	GCACCACTGC	ACCCTGGCAA	TCTCATGCTC
32051	TTTCTTTCAC	GCCTTTCCTC	CTAGCTCCTC	TCTTTAATCC	TTTGCCTTGT
32101	CTTCTCCTTG	ACACCTTATC	CACAGAGAAA	CAAACATATA	TCCCCAAACC
32151	ACAGACACAC	AGATGTGTGT	GCACGTGCAT	GTGCATGCAC	ACACATCTGC
32201	ATGAACATAC	TCACACATGT	CCAAACGTAG	TTCAGAGCCT	GGTTTAGGAA
32251	AAAAAAAAAA	AAGCATAAAG	ACCAAGCTTC	AAGACACCTG	ATTTTCATGC
32301	CAGTTCGATT	TCTAATCAAT	TAACCTCTGA	TTCTGTTATC	TTGAAAAAGT
32351	CATGTATCCT	CTCTGTGTCT	ATGTTTCTCC	ATTTTTAAAA	ATGAAGGTAA
32401	TAAACTCTCT	CCATCTGAGT	TAAATGGAAT	TGTAGTACAA	ATATAAGAAC
32451	CAAATAGGTG	GCTGGGCTTG	CCGTCTCATG	CCTGTAATCA	CAGCGCTTTG
32501	GGAGACCAAG	GCTGGAGGAT	CGATTGCTTC	AGCCCAGTTG	TTTAAGATCA
32551	GCCTGGGTAG	CACAGTGAGA	TGCTGTCTCT	ACATTTTTTA	AAAAAATTAG
32601	TCAGGCGTGA	TGGCTAATTA	AACACTTCAG	GAGGCTGAAG	TAGGAGGATC
32651	TCCTGAGCCT	GAGAAATTGA	GGCTGCAGTG	AGTTTTGATG	GTACCCCTGC
32701	AATCCAGCCT	GGGTACAGA	GCGAGACCCC	GTCTGAAAGA	AAGAAAGAAA
32751	CAGAGAGAGA	GAGAGAGAGA	GAGAGAGAAA	GAAAGGAAAA	GAGAAGGAGA
32801	GGGGAGAGGG	GGAGAAAGGG	AGAGGGGGAG	AGAGGGGGAG	AAGGGGAGAG
32851	GGGGGAGAGG	TGGGGAGGGG	GGGAGGGAGG	GAGGAAGGGA	AGGAAGGAAG
32901	GAAAGGAAGG	AAGGAAGGAA	GGAAGGAAGG	AAGGAAGGAA	GGAAGGAAGG
32951	AAGGAAGGAA	GGAAGGAAAG	AAGGAAGGAA	TCCAGATAGG	TGCTATCAAG

FIGURE 3L

33001	TAAAGCCACA	GAGTTGGGGA	GGCTCTAAGG	TTAATGGGTT	ACAATAGTGA
33051	GCATGGGCTG	TCAGACATGC	ATCATCCTAG	AACGGCAGTG	TTATTTTCTC
33101	TGGATCATGT	TCCTGGAGAC	TTCCCAGTCA	TTTGGGGGCC	ACTGTTAGAT
33151	ATGTGATGAC	TTTACAGACG	TAGACAACTC	CCCAAAGGTA	AGGAAATATA
33201	TGAATCTCTT	TCAGTACCTT	GGAAGAAAGG	GTTTATATAA	AAACACAAAG
33251	CCCCATTTTC	AAAAATCCAT	AATTGATTTT	AAAAAATTAA	ATGGTGTCTT
33301	AAAAGGCTAA	ACTAAGCTTT	TAGATCTCCC	AAAGAATTAA	GAAAGGTTGC
33351	AGACATTTTT	CTCCAGTGTA	GAGTCATTGA	TTTCTGATAC	CCAGTACAAT
33401	TTATAGAAAT	ATCATCTGCT	AGTCAAAACC	CTCCTGAAAC	TGTCAGCTCA
33451	CACCGCTCAG	CACTGTCACT	TCAAAGGACT	CCGGCAGGCT	CTGGCTTACT
33501	CAGCTCTTAA	TGATGTCTTC	CTGATTATGT	TTACACAGAGT	GAAACTTCTA
33551	CCCGTCAATT	TTAAACTAAT	TTTATTATGG	AATAGTTAAA	ACATTCAAGA
33601	GTATATATAA	CATATATGTA	GATCAGTGAT	TCTCAACCAG	GGAGCAATTT
33651	TGCTCTGCAG	GGGACATTTG	GCAATGTCTG	GAAACATTTT	TTGTTTTTCA
33701	AGCTGGGGGT	GGGGTGGTGG	GGGGTATCAC	TGGCATCTAG	TGGGTAGAGA
33751	CCAGGGATAC	TGCTAAACAT	CCTACAGTGC	AGAGGACAGC	CCCTGCAACA
33801	AAGATTTTTT	CAACCCAAAA	CATCTGTAGT	ATCAAGATTA	AGAAAGCCGA
33851	TGTAGGTAA	GAAGCTTAAT	TTACTTTTAG	AGACAGGGTC	TCCCTTGGTT
33901	GCCCAGGCTG	GAGTACAGAG	GTGAGATTGT	CTCACTGCAG	CCTCCAACCTC
33951	CTGGGTTTAA	GTGATCCTCC	TGCCCTCAGCC	TCCTGAGTAG	CTGGGAATAC
34001	AGGTGTGTGC	CACCACACCT	GGCTAATTAA	AAAAAAAAAA	GTGTAGAGAC
34051	AGAGTCTCAC	TTTGTGCCCC	ATGCTGGTCT	CAAACCTCTG	GCTTCAAGAG
34101	ATCCTCCTGC	CTTGGCCTTC	CCAACCTGCTG	GGATTACAGG	TATAAGCCAC
34151	CGTGCCCAAC	CAATTAAGAA	GCTTAATAAC	GTGAACTTCA	TAACCTGCTA
34201	CCCAGTGTA	CAACTAGAAC	ATAATCCGTA	CTGTCCTATC	AACTGTGTCC
34251	CTTTCCCATC	AACCTGCCCC	TCCAAGTAGAA	GGCCTTCTAC	CAAAATTTTT
34301	TTTTCTTTTT	TCATCAGTAT	TCTCATATCT	TTTTAAAAAT	AATCCTTTTA
34351	CATTTTAGAG	GTATTCTTAA	AAATATTTTT	TTGTTTTACT	TGATTTTAAG
34401	GGTTGTTTTT	TTTTGAGACG	GAGTCTCGCT	CGTCGCCCAG	GCTGGAGTGC
34451	AGTGGTGCGA	TCTCAGCTCA	CTGCAAGCTC	CGCCTCCCAG	GTTACACGCCA
34501	TTCTCCTGCC	TCAGCCATGA	TGTTATATTG	CTTCTAGTCT	TCTGTGACTT
34551	GGCTTTGTTT	CATTCAATAT	GTTACATGTT	TCTAAGATTTC	ATCCATGTTG
34601	ATCTGTTTAG	CTATACTTTA	TTTTCTGTTA	GTGAATATTT	CATTTTTTTT
34651	AATGTCTATA	GCTTTGCAAT	AATACTTGAT	ACCTTGAGAG	CCAAGTCTCC
34701	CAGCCTATTC	ATCTTCTTCA	TGAGGATACA	TCAGATAAAC	CTAGTTTAAG
34751	GGACATTCTA	CAGAGTAACT	GACCTGTACT	TATTGGAAGT	GTCAAGATTT
34801	TAAAAGATAA	AGACTGAGGA	ACTGTTCCAG	ATTAAAGGAG	ACTCCAGAAA
34851	CCTGCCAACT	AAATGTAACG	CATGGTCCTA	GATTGGATCT	TGGGGGAGAT
34901	GGTGCTCTAA	AGAATACTGT	AGGGACTATA	GGTGAAATTT	CAGTAGGGAC
34951	TGTGGATTAG	ATAGGGGTAT	TGGATGAATG	TTAAATTTCC	TGATTTTGAT
35001	AATTGCACTG	TTGTTATGTA	AGAGGATACT	TTGGTTCTCA	GAAAATACCA
35051	ACATAATTAT	TTAGGGATGA	AGAGTCATGA	TATCTACAAT	TTACTCCCTA
35101	ATGTTTCAGA	AAAGATATAG	ACAGACAGAC	AGACAGACAG	ACAGACAGAT
35151	AGATAGATAA	AATAACGAAA	CAAAAGTGAC	AAAATATTGG	CGATGGATGA
35201	ACCTGTTTGG	AGGATATAAG	AGAGTTCTTT	ATACTGCTGC	AACTTTTCTA
35251	TAAGTTTGAA	ATTATTTCAA	GATTAAGAGT	TGCCTCCAAA	TTGCGAAATC
35301	CTTGCTGTTT	CATCAAAGTT	AGTGTAAGAC	AGCACTAGCC	TAATATGTGA
35351	TCAGTGTTTG	TAATTTCTTC	ATGTGTGTTT	GAGAAGAATG	TGTGTGTCCA
35401	CCCAAATGTT	GAGTGCTGCT	GGGGTTTTTT	TTTTGTTTTT	GTTTTTGTTT
35451	TTGTTTTTTT	TGAGACAGAG	TCTCACTCTG	TCTCCATGCC	TGGAATGCAG
35501	TGACTCAACC	TCGGCTCACT	GCAACCTCCA	CCTCCTGGGT	TCAAGCGATT
35551	CTCCTGCCTT	AACCTCCCAA	GTAGCTGGGA	TTACAGGAGC	ACACCATCAC
35601	ACCCGGCTAA	TTTTTGTAAGT	TTTAGTAGAG	ACGGAGTTTC	GCCATGTTGG
35651	CCAGGCTGGT	TCGAACCTTT	AGATGTCAGG	TGATCAGCCT	CCCAAAGTGT
35701	TGGGATTACA	GGCATGAGCC	ACCGCGCCTG	GCCAAGTACC	CATTTTTTACA

FIGURE 3M

35751	TATGTTCAAA	AATTCAAGGT	TGCTAATTAT	ATTATCCAAA	TCTTCTTTAT
35801	ATTATTTTGT	TCTTTTAAAC	CTACCAATGA	AAGGTGTGTT	GAAGTCATTC
35851	ACTATATTGT	TGATTTGTCA	GAATTCTATC	CACTTTTGCT	TTATATGCTT
35901	TGAAGCTATT	TTCACTAAGG	GCAAAATAAT	TTAAGACTGC	TCATTATTCC
35951	TTTGTACACT	TTAGTTACCA	CTTTCAGAAT	AATTTTCATT	TCTCCTGAAA
36001	TACATCTTTT	AGAGTGTTTT	GTTTTGTTTG	TGTGTGTGTA	GGCCTGCTGG
36051	TGGCAAATTC	TTTCGTTTTG	TTTTTCAGAAG	ATAAACCCCTA	ATTATTGAAA
36101	GGTGGTTTTG	TTGGGGATGT	GATTCTAGAC	TGACAGTTAT	TTTCTCTCAG
36151	AACTTTGAAG	ATGTCATTCC	CCTTCTTTGT	CTTCCATTGT	TGCTGTCGAG
36201	GAGTTTGCTT	TTAGCCTTAT	TATCTTCCTT	TTGCAGGTGA	TCTCATTTTC
36251	TCTGGATGTT	TTAAAGACTT	TTTTCTTTGC	CTTTATGATT	ATGCAGTTTT
36301	CTCTAGGAGT	TGTCCAGTGT	GGATTTCTTT	TTACTTACCC	TGTTTGGTAT
36351	ATCTTGTGTT	TCTTCCATTT	GTGAATTTCAT	GTCTTTCATC	AGCCATTTTC
36401	TTTTTGAATA	TTGACTCTAT	TCTATTCTCT	CTCTGTAGAG	CTCCAATGAA
36451	AGACTATTAG	ACCACATTCT	TCTGTTATCC	ATTTCTCTTC	TCTCCTTCAT
36501	ATTTTCCATT	TCCTTAACTT	TCTGTGATGC	ATTCTGGGTA	ATTTCTTCAG
36551	CTCATCTACC	AGTCTTTTAA	GTCTCTCTTA	AACTATGTAT	TAGGTTGGTG
36601	CAAAAGTAAT	TGCAGTTTTT	GCCATTAAAA	GTAATGGCAA	AACCATAGTT
36651	GCTTTTGCAT	CAACCTATAT	CTCTTACCTT	TTTACCACAT	ATACAAAAAT
36701	GTATGTTATT	CTATGAATAA	GTGTTTCATG	AATTTAACCA	TGAGCAACAA
36751	TGACACAATA	TAAAAATGCA	GTTATAAGTC	AAAATTATTG	TTATTACTCT
36801	TATTCATTCC	ATTTGATTGT	TGTTTTCTCG	GTAAAACTAA	AAATGTAATG
36851	TAGAAATAGA	ACAATATGCA	TCTTCCATTG	AGCTCACTAT	ATTTGTTTAC
36901	CCTCAAAGTA	ATTGCTAGAC	CTTGGGTATT	TACACTGAGA	TCCCTCTCCT
36951	CCCATTTTTT	TCTTTTTCTT	TTTCTTCTCT	TCTCTTTCTG	CTACCTTTTC
37001	GAGAAGATTT	CCAGTTGACA	AAGAATGAAA	AAGAAAGAAT	AATCCTATTC
37051	TGCTAGGCCA	TGCAACCCCA	TAGGGTCCAA	AGTGAATGCC	CTTGAGGAG
37101	GATAGTGACA	CTGGGTGAGC	ATTAGTGCAT	TTGTCTTAAA	GAAACCAATT
37151	ATAACCCGTA	GTGCAGAGCC	TCTCCTTCAC	AATGAGGCCT	GGTGGCAGCA
37201	TGTGCAGTAG	GGGGCCAGAG	CAAAATAACA	GGGGCTCTAG	TTAATTATGG
37251	AAAACCTTGCA	ACTAGGACAT	ATTGGTTATT	CCCAAAGCTC	CCAACCAACA
37301	TTCTCTCATC	TTCTGACGTC	TTTTCTTCTC	TCTCTTTCTG	CTACCTTTTC
37351	AGACCTTAAA	AGATTCCATT	AGTGACTTTA	GTGAGAAAAA	TGCAATATTT
37401	TAGGATTATT	AAATGGTGTG	GTTTTTAGTT	TTTTGTATTG	TGTTAAAATA
37451	TACATAAAAT	TTACCATTCA	TCACGATTTT	CAGGTGTACA	ATTCAGTGGC
37501	ATTCAGTACA	TTACACATTGT	TGTGTAACCG	TCACCACTGT	CCATCTCCAG
37551	AACTTTTCAT	CATCCCAAAC	TCAAACCTCTG	CACGTATTAA	ATGATAATTT
37601	CCCATTACCC	CCTCTCCTCA	GTCCCTGGTA	ACCACGATTC	TGCTTTTTAT
37651	CTTGATGAAT	TTGACTATTC	TTGGTACCTC	ATATAAAAGT	GGAATCCTAC
37701	AATACCTCTT	CTGTGTCTAG	CTTGTTTTGC	TTGGCATAAC	ATTTTCAAGG
37751	TTTCATCCATG	TCGTAGTACA	CTGAGTTTTT	CAGAAGCATT	TATTTTCAGTA
37801	CACAAGGTCA	TCTATTCAGT	ATCAGTTTTCA	GGCAGCTGCT	GGTGTTAGGA
37851	CTAGAGAAAG	TTGTCTCTGC	CTAACAGATC	ATTTACTGTC	ACATTTCTCG
37901	CTGCAAACTT	CCAAATATAA	AAAGGGTGGT	CTAGAGAAAA	GCAAGTGAGA
37951	ATGTCATGTC	ACTGCCATAT	ATTACGTTAT	TCTGAATTAA	CTTCAACAGT
38001	AAGAAATGAA	ATACTGATTC	ATTTCTCCCA	ACAACATTTT	GATATTCTCC
38051	TTGCACCTCC	AAAAAGCCTA	AAACTCCCGA	GATGGATTTT	TTTTCTCCAG
38101	GGAAGTGCCTA	AGGAATCTGA	GGAATCTTTC	CCCCTCTTAT	GGAAGAATTT
38151	GTTTCATGCTC	AGAATAGAGA	AAAAGTAGGA	GGAGAACCAG	AAAGAGGAGA
38201	AAACATCTAA	GCAGTTTCCT	CTAACTTGAC	TGAAGAACCA	CATTTGGAAC
38251	AATAAAATGA	CCCAGCACAT	CTCTCCCTTC	TGGAAGGGTT	TAATGTTTGA
38301	TGTCACAGGG	TCTTTTCTCC	CCTGCATATG	AATTTCCCTT	TCGTCTACAC
38351	GGGCTGCCCC	ACGGGTATCT	CCACACAGCA	GAAATCCTCA	GAGAAGCTTA
38401	AAGATATGTA	GGGTAAGAGG	AGCCCCAGGA	ATGAAGATTT	AAGGACAAAA
38451	CAGAAAAATA	AAAGGAAATA	GAAGCTGGTT	CCCTATCTGG	ACTTGAATGT

FIGURE 3N

38501	TCAGAATATT	TAAAATGTTT	GCTTTAAGAA	TAGTCTGTGG	TGGGCAAAAT
38551	AGATGATAGC	CACATGACTT	GTATTCCTAA	GGGTAAGAAG	CAAATTAATA
38601	AAAAGAAACA	GTTCTGAACA	GAAATGAAAA	AATAAGATAA	ATTGCATAGT
38651	TCTTTTTTTT	TATTAGATGG	AGTCTGGCTC	TGTCGCCCAG	GCTGGAGTGC
38701	AGTGGTGCGA	TGTCGGCTCA	CTGCAACCTC	CAACTCCCCG	GTTCAAGTGA
38751	TTCTCCTGCC	TCAACCTCCT	GAGTAGCTGG	GATTACAGGA	ACACACCACC
38801	ATACCCGGCT	AATTTTTGGA	TTTTTGGTAG	AGACGGGGTT	TCACCATGTT
38851	GGCCAGGCTG	GTCTCGAACT	GACCTCATGA	TCTGCCCGCC	TCGGCCTCCC
38901	AAAGTGCTAG	GATTACAATG	CTTACACCTA	GAACAGATCT	GTCACCTTTC
38951	AAACTTACAG	TGTGGGCTTG	TTTTGTTATC	AATGCATTGA	TATTTACAGT
39001	ACCTATGGAT	AGTCCATGTA	CTGAAATAAA	ATTGATTTAG	GAATTTTGTC
39051	TTATAAGTGT	TCTAAAGACT	TGCACAAGTG	CACACATACA	CACACTATAT
39101	ACATAGTGTG	TGTGCATGTG	CGTGTATATA	AATGAGTAAC	CTTAGACTTA
39151	GATTTGTTAG	ATGAGGAAGG	TTTCAACCTT	CCCCAAAATG	CAAATGGAGA
39201	ATTTCAACCA	TATAAACCAA	ATATTGGCAT	TTTATCTCTG	GAACACAAAC
39251	ATCTTGTTGT	ACTTTATGGT	ACTTACGTAA	TGGCCTGAAT	GCTCTAGTTT
39301	TTGCCAATAT	ATTTTACATA	ATTTTGTATA	CAAGTTTAGT	GGTATAGAAG
39351	ATAAGGACA	CTAAGCAGGA	TTAACAGCTT	GGTTCCTAC	AGCTGTTAAG
39401	TATGAAACCA	CACCATGAAA	AGGCAACAAG	CTTCTTCCAG	GCAATGGAAG
39451	GCTTTTTTGG	GGAGAAAAGA	AAGTGAATTA	CAGGTTTAAA	CCTAGGAATG
39501	TCATTTTTTG	AAACTTGTTT	AAAATATTTT	CAATCCTTCT	AGTGGTTTGT
39551	GAGCTCCTGG	GGTTTCTGGA	AGGTGTTTGG	GAAGTGGATA	GAGGGTTAGT
39601	TCATGCCTTT	AAAAGCCAAT	ACATTTCCAT	TTCTCTTTTA	TAACCAAGTA
39651	ATAACCCAAT	TATGCATGTA	TTTTATATAC	ACAGACACGT	ATTTATTTTT
39701	ACTCCAAAAC	AAAATGGTCT	GAGGCCTTTC	AAGAAAGTGC	ATGTGGCGAA
39751	GTCATGGGGG	GCAGGGTGGA	GACCATTGGG	TGGTGCCAC	TAAGTAGGTT
39801	TCTCAGTTGG	CTTATCTCTT	AGTGGACCAT	TGCTAGCAAC	CAGGGTGTTT
39851	TTAAGCATT	GACAGTTTTT	CATCACTTTT	ATTTGCCTTC	ATATATTGTT
39901	TCATTTACAC	CCTTAGTATC	TCTTGTTTTA	AAGACAGGAG	ACAAAAAGAA
39951	CATGGATATT	TAAATACAAG	TTAATGAGGA	ACTTTAAAAT	AATAATAATT
40001	CTACAAATTT	ACCTCAAGAT	ACTTTACCAA	ATTCATAAGT	TACATTTATC
40051	TGATCAAAAT	TCTTGTTGCA	CATATCAAGA	TGTTTCTTAT	ACAGCAGAAA
40101	TCAGTAGAAA	AGAAAAAATA	GGCCAAGCGT	GTGGTGGCTC	ACACCTGTAA
40151	TCCCAGTACT	TTGGGAGGCC	AAGGCAGGAG	GATTGCTTGA	GGTTTGGAGT
40201	TCAAGACCAG	CCTGGGCAAC	ACAGTGAGAT	CCCATCTCTA	TTAAAAAAT
40251	TAGAAAAGAA	AAAGAATAAA	ATGGGGCTGT	TATATCCAAA	TTGGCTTTTT
40301	AAAAATCAGC	AATAAGGCCG	GGTGTGGTGG	CTCACACCTG	TAATTCCAGC
40351	ACTTTGGAAG	GCTGAGGCAG	GCGGATCAAT	TGAGGCCAAG	AGTTTGAGAC
40401	CAGCCTGGCG	AACATGGTGA	AACCCTGTCT	GTAATAAAAA	TACAAAAATT
40451	AGCCAGGCAT	GCTGGTGCAT	GCCTGTAATC	CCAGTTACTC	AGGAGGCTGA
40501	GGCAGGAGAA	TCACCTGAAC	CTGGGAGGTG	GAGGTTGCAG	TGAGCTGAGA
40551	TTGCACCACT	GCACTCCAGC	CTGAGTGACA	GAGTGAGACC	CTGTCTCAAA
40601	AAAAAAGAAA	AAAAAAATTG	GCAATAAAAA	CAACCTGTTG	CTTGCTGGAG
40651	GAAAAACCTG	CTTGCAAAGC	TCAGTCTGAT	ATCATTTTTT	AAACAAAAC
40701	CTAAGAACAA	GCCAGTCAGT	TAAGCTAAAA	CCAAATATTT	GATTATGAAA
40751	AGGGTTTTTG	TATATTTTTA	CAGGATAAGA	TACAAATAAA	TTTCAGTCTT
40801	TCTTTTAATA	TGTATTTCTG	TTCCCAAACC	AGACACAAAG	CAATTTTTAA
40851	ACTTGATCGT	CAAGAAATCT	GTTTTCTCCT	ACACAATCAA	TGAAAAGTAA
40901	TCTAAACAGT	GTTTGTGAGG	CCAGGCACAG	TGGCTCACAT	CTGTAGTCCT
40951	AGCATTTTGG	GAGGCCTAGG	CAGGTAGATT	GCTTGAGCCC	AGAATTTCAA
41001	GACCAGCCTG	GACAACATGG	CGAAACCCCA	TCTGTATTAA	AAAAAAAAAA
41051	AAAAAAGAC	CATATGTCTG	CAGTCAGATG	GAAAAAGTAA	AAATATGTAA
41101	TAAACACATA	TGAATAATAT	TAAGGACCAT	ATTTTAAAAT	AAACTTGATA
41151	ATAAATTTTT	AATAATTTTA	TCTACGATAA	AATGTTTTAC	TTAAATTTTC
41201	TTCTTTATCA	TGCCACACAA	AAATGGCAAA	ATGATTAAGA	GAGTTTGCAA

FIGURE 30

41251	AATTATGTGG	TATAGTGAAA	GAGGTTTGCG	GTAAAAA	AAAAAGAGAG
41301	AGAGAGAGAG	AAGTATGGGG	CCATGGGGAT	AGTCTCTGTA	ATCAGTCACC
41351	TGAACCACTT	TTAATACTCA	AAAGACTTAT	GAGAAATAAA	ATCTGATTTT
41401	TGCTAAGATT	TATTAGCAAA	ATAAATCTTA	CTCCTTCCTG	TCCCTCTCTA
41451	ATTATCCTTC	AGCTTGACCA	TGTATGAAAG	AAAATTTACA	TTTCACTGTT
41501	TAATCTATTT	AAAGATGAAC	ATTTCCCAT	AAATCAGGAT	GCACCTTATA
41551	ATCAGTAGCA	TCTAACAAATA	TAAGTCAGCC	AGGCTGCAGT	TGTGACTGTA
41601	GTTAGAATTG	CACATGTGTG	AACATCAAAT	GAGCCAGCAT	CAAAACGTGC
41651	AGAATGGCCA	GGCACAGTGG	CTCACACCTG	TGATCCCAGC	ACTTTGGGAA
41701	GCTGAGGTGG	GTGGATCACT	TGAGGTCAGG	AATTCAAGAC	CAGCCTGGCC
41751	AAGATGGTGA	AATCACGTTT	CTACTAAAAA	TACAAAAATT	AGCCAGGCAT
41801	GGTGGCAGGT	GCCTGTAATC	CCAGCTACTT	GGTAGGCTAA	GTCAGGAGAA
41851	TCGCTTGAAC	CTGGGAGGCG	GAGGTTGCAG	TGAGCTGAGA	TCGCACCACT
41901	GCACTCCAGC	CTGGGCGACA	GACCAAGATT	CCACCAAAAA	AAAAAAAAAA
41951	ATTGCAGAA	TGGTGTGAGC	GACTTGGAAG	AAAATTCTGC	AAAGAAAAGT
42001	CCTTTTTTTT	TCTTTTTTTT	TTTAACTCC	TAGGAACCAA	ATGGTTGTGG
42051	AGAAGGAGTA	AATCAGACAT	GTTTAGCAAC	ATTCTTTAAG	CAGGAGTCAA
42101	AAGTAAGCTA	ACACTACATA	ACTGCAAGGC	CAGCTTAGGA	GCCCAGGACC
42151	AATGACTCTC	TGTTGTTTTA	TGGATTATTT	TAAGAAATGC	TGCATCATCA
42201	AATTCTTAAT	ATAGAGGATG	ATACATGGGT	AAGTGTAGAC	ATCAAAGAGT
42251	CTGAGTCAAA	TGCTGAATGT	GAAAAAGTTT	TAGGAATACC	GAAACCAATT
42301	TATTTTGCTT	AATGTTTCTC	TTTTTCGTGT	ACAAGTATGC	TATATGAGAA
42351	AATAATCTCT	ATTTAATTAA	ATTTATAACA	GCCCTTTCAA	TAAGTATAAA
42401	ATGAACATTC	TGATCATGTC	ATAGTTTAAC	TTGCATTTTT	TTGTCTTAAT
42451	GGCAAAAAAC	CAATGACGCT	TCTTACAATG	ATAGCATCTT	AGACTCAATG
42501	AAAAGTGGGG	ATGAAATGAA	ATTTGGGGAT	ACAGTACTTT	CCCCTCTTCT
42551	CCTAAAACAG	ATAATGAGCT	TGAATGATCT	ACAATGTTTG	CTAACTCTAC
42601	TGCTTTCCTA	ACTGCTGCTC	GTGGTGTTC	ATTTTAATAA	AAAGCTGTGG
42651	GCTGTTCTTA	TTTTGTTTGA	CATAGGGACT	TTTTTTTTTG	CCCAAGACTT
42701	TTAATATCAT	GTGGTCCGTA	TTTAACTCTC	CCTAAAATAT	TTCTTGGGAA
42751	GAGAAATTCT	AGTAGTTCAG	TTTCGCTTGT	ATGATTTCTT	TCAAAGGTGC
42801	TATTTACTCT	TATTTCTTTT	GTTAGGGGTG	CAGGCTGCAT	CTTTATTGAA
42851	ATGTTCCAGG	GTCAACCTTT	GTTTCCTGGG	GTTTCCAACA	TCCTTGAACA
42901	GCTGGAGAAA	ATCTGGGAGG	TAGGAGAATA	ATTCTTCTAA	AGAAAATGAA
42951	ATATCTGCAT	TTTAAGTTTT	GAACCAAATT	TGCCTTACAG	ACAAATGAAG
43001	CAGTCCATCT	GCTCTGAGAT	ATTAAGCCCT	ATATTAAGAT	TGTAGAAACT
43051	GTAGCATTTG	CCACAGCTAT	AAGCACCTG	GGAATGTGTG	GTCAGGAAAC
43101	TCCCTGTTGC	CCCATAGCAG	CCCATGAATC	CAGCTCACTG	AATGATGTTT
43151	AGGTCTCCTG	CTCCCTGTCA	TTAGTATTGT	CTTAACCTCC	CAGGGCAATT
43201	TCTGCCATTA	CTACTCAGAC	ATGTCCCTAC	CTTGCTACCT	CCAGTTCTAA
43251	TGCTACCATA	TATTTGGCCC	TGGATCTTTG	TCAACTGAAA	ATAAGACATA
43301	GAATTTTGTG	CTGGGTGCAG	TGGCTCATGC	CTGTAATCCC	AGCACTTTGG
43351	GATTGCTTTG	AGCCCAGGAG	TTTCGAGACCA	GCCTGGGCAA	CATGGCGAAA
43401	CCCCATCCCT	ACAAAAACAA	AAATGAGTGG	GCTGTGTGGC	GCACACCTTA
43451	GTCCCAGCTA	TTCAGGAGGC	TGAGATGGGA	GGATCACTTG	AGCCCAGGGA
43501	AGTCGAGGCT	GCTGTTAGCT	GTGACCACGC	CACTGCACTC	CAGGCTGGGG
43551	AACAAAAAAA	AGACACAAAA	TTTTCATAGA	ACCCTGATAG	AACAGAGGCT
43601	TTCCCTCTTA	GTGTGAAAGA	AGTGTACCAT	TTATCATGCT	TATCCACAGC
43651	CAAATTCCTA	AAGTGTC AAG	GTGCCTTTGT	GTGTGTATGC	AGCTCCATTT
43701	CTTAATTCAT	TATTTATCCC	TACCGCAGTT	GCCTATGATA	TGCTTTGTTT
43751	TTATGGCCCT	TATATAGTAT	TACAGTCATA	CTATAGTCAT	CTGTATATTT
43801	CCTTTTTTGG	TCATATTTTT	ATTGTGGTAA	AATATACAAA	ACAAAATTTA
43851	CCGTCTTAAC	CCTCCTTAAG	TGTACAGCTT	GTCAGCATTA	AATACATTCA
43901	TATAGTTGCA	CCACCATCAC	CGCCATCCAT	TTCCAGAACT	TCTCTATCAT
43951	CCCTAAGGGA	AGCTCTGGAC	CCACTGAACA	ATAACTGCCC	ATCTTCCCTC

FIGURE 3P

44001	CCCACACTCC	CCTAGCCCCT	AGTAACCTCT	AATCTACTTT	CTGTCTCCAT
44051	GAATTGGCCT	ATTCTAGGTA	CCTCATATAA	GTGGAATCAT	ACAAATTTGT
44101	CTTTCCGTAT	CTGGCTTATG	TCACTTAGCA	TATTTTCAAG	GTTCATCCAT
44151	GTTGTAGAAT	GTGTCAAGGG	GCTTTAAATC	GGCGGGGTGC	AGGGGGGTAC
44201	TTTATTACTT	GCTATCCTGG	ATCCTGCTGC	TTGTCTTCTG	GCTAAAATAA
44251	AATGTACTTT	GTGAAATTAA	GACATTTTAT	AGAGATTAAT	TACTGACATT
44301	AAATTTTCTT	CTAGAAACAT	GGGGGCTATT	ATGAAGGAAC	ATGGGAAAAA
44351	CTGGGAAGCA	TTCACTCACTG	AAAAAAAAAA	ATCCAAGCCA	AAAGACTTTT
44401	TCTAAAAACT	TTCTTGCAAG	ACAGAGCAAT	GCTATCTTCA	CATTATGTTA
44451	TTGGGTGCTA	TAACATCATC	TAAGCTGGAG	ACAGCCTACT	GTCATAGCTT
44501	TGGAGTCCAA	AGACCTGGGT	TTGAATTCTA	ACCATTTTCT	AGCTAAATGA
44551	ACATGGGCAA	GTTATGTAGT	CCCTCTGAAC	TTTCGTTTCC	TTGTCTGTAA
44601	AATGGCAACA	ATGATAATAA	GGACTTTCTA	ATTCTTTATT	GAGAATTCCA
44651	TAAAAACAAA	TGCATAACAA	GCTCCATGCA	CCATAAATGC	TCAATAGATG
44701	CTTGCTTTCT	TCCTGTCCCA	TACAAATTGT	TGTACAGATG	TTTCAATAAC
44751	CTAACTGCTA	GCAAGTATTA	CCTGAAATTT	AACCCGATTG	TTCTCTTCTT
44801	TCACCTTAGCA	GTATTATTTT	TTGTCCACAA	TAGAGGAAGC	ACAATTGCAG
44851	TTCTGATGCT	GCAATGACCT	TTTATACATT	TGAAGAGTTT	TTCTTGGTCA
44901	TTTAATCAGG	AAACAACACT	TACTCACCAT	ATATGAGGCG	AGTAACTCTA
44951	CAAGACTCTA	CAAGGTCTTG	TAAGAAAGCTA	TAAGCCAAGG	GGGAAAAAAA
45001	AAAGAAGAAT	AAGAAAAACA	CATGATCTGT	ATTTTCAAGT	GTTGTTTCAGT
45051	CTAGGTAGGG	CGATGGGTGA	AGTATACGTA	AATATATGTG	AAACAAACAT
45101	AAACTATGTA	TATATGTAAA	AGGATGTATG	TATAGATAGT	TAATATAAAT
45151	TGTAATACTG	AAATAAGATG	TGCTATTAGG	ATACTTGAAG	AGTAGTTTAT
45201	TTGAAAAGAA	TATAAGTATA	TCCTTGTGTG	CCATTAGTAT	TTGAAGAGTT
45251	GTATATAAAC	TGATTTTTTT	TCTTTTTTCT	TTTTTTTGAAG	AAGGAGTCTT
45301	GCTCTGTCAC	CCAGGCTGGA	GTGCAGTGGT	GCCATCTCGG	CTCACTGCAA
45351	GCTCCACCTC	CCCAGTTCAA	GCGATTCTCC	TGCCTCAGCC	TCCTGACTAG
45401	CTGGAATTAC	AGGTGCCCGC	CACCACACCT	GGCTAACTTT	TGTATTTTTA
45451	GTAGAGACGG	GGTTTCACCA	TGTTGGTCAG	GCTGGTCTCA	AACTCCTGAC
45501	CTCGTGATCC	ACCCGCTTTG	GCCTCCCAA	GTGGTGGGAT	TACAGGCGTG
45551	ATGCCACGCG	CCCAGCCTCA	TAAACTGATT	TTTAAAATAC	AATATACAGT
45601	TAGGCATAGT	TGTGTGTGCC	TATAGTCCCT	ACTGCTTGGG	AGGCTGAGGC
45651	AGGAGGATCC	TTTGATCCCA	GGAGTTTGGG	CAACATAGTG	AGACCCCAT
45701	CTCTAATAAT	AATAAATATA	AATTTCAAAT	AACATTTTAA	AATATGACAT
45751	ACTATCTTTG	AATGACCACA	CAATTTAAAA	AGCAATCATT	TTACGGTTCT
45801	TTAGTGTTCA	GTTAGCACAG	CACTTAGAAA	TCATAGAATA	AAGTGAGCAA
45851	GATGCTTCTC	AAAGCCTGAT	CACTCTTTAG	GA CTCACAAT	GGGCTAGGTA
45901	CTATGCTGGA	AAGAGAAAAA	ATAATAATTT	TCTAACCTGC	TTGAGACATA
45951	GTGGTATAAA	TGATAACACA	GCTGCTGAAC	GTGATGACTT	TCTCACTTTG
46001	TCCGCAGAGC	AAGAAACTAT	AGATGCAGTA	ACAAAACCTGC	ATTCAATGAA
46051	CATGGGACTG	TAGATAACAA	ACTAACTTCA	TTTCTTTGGG	TACATGCCCT
46101	GTATTGGGAT	TGCTGGATCA	TATGGTAGTT	CCATTTTAA	TATTTTGAGG
46151	AACCTCCATA	CCATCTTCCA	TAATGGCTGT	GCTATTTGCA	TGCCCACCAT
46201	CAGTGTGCAA	ATGCTCCCTT	TCCTCCACAT	TCTTGCCAAC	ACCTCTTTCA
46251	TCTTTTTGAT	AATAGTTATG	AGGCAATATC	TCACCATGGT	CCTAGACTTC
46301	ATTTGTCTGA	TGACTAATGA	TATTGAGCAT	TTTTTCATAT	ATCTCTTGGC
46351	CATTTGTAGG	TCATCTTTTG	AGAAATGTGT	ATTGAGGTTC	TTAGTCCATT
46401	CCTGCTACCA	TAACAAAATC	CCTTAGAGTG	GGCATTTTAT	AAAGAACAGA
46451	ATTGGCCCGG	GGCGCAGTGG	CTCATGCCTG	TAATCCCAGC	ACTTTGGGAG
46501	GCCAAGGTGG	GTGGATCACC	TGAGGTCAGG	AGTTCAAGAC	CAGCCTGGTC
46551	AATATGGTGA	AACCCCATCT	CTACTAAAAA	TACAAAAACT	AGCCGAACGT
46601	GGTGGTGTGC	ACCTGTAGTC	CCAGCTACTT	GGGAGGCTGA	GACAGGAGAA
46651	TTGCTTGAAC	CCAGGAGGAG	GAGGTTGCAG	TGAGACGAGA	TCGTGCCACT
46701	GCACTCCAGC	CTGAGCAACA	GAGTGAGACT	TCATCTCAAA	AAAAAAAAAA

FIGURE 3Q

46751	AAAAAAAAAA	AAAGAACAGA	AATTTATTTT	TCAGTGTCT	AGAGGCTGGA
46801	AAGTCCAAGA	TCAAGGCACT	GTAAGGCTGT	GTCCAGTGAG	TATATTTGGT
46851	CTCCAAGTTA	GTGCCTTGTC	GCTGCATCCT	CCAGATAGGG	CAAATGCTGT
46901	GTCCTTACAT	GGTGGAAGGG	TAGAAGAGCA	AACGGGCCTG	ACTGATTCCC
46951	TCTAGCTCCT	TTATAAGGGC	ATTCATCTCT	GTCCTTGTGT	CCTAATCACA
47001	CGCTAAAGGT	GGCTAAAGGC	CCCACCTCTT	AATACTGTTG	CATTGGGGAT
47051	AAAGTTTCAA	CATGAATTAT	GAAGAGAATA	CAAACATTTA	AACCACAACA
47101	AGTCCTTTGC	CCACTTTTTT	TTTGGAGACC	GAGTCTCACT	CTGTTGCCCA
47151	GGCTGGAATG	CAGTGGCTTG	ATCCTGGCTC	ATTGCAACCT	CCACCTCCTG
47201	GGTTCAAGCA	ATTCTCCTGC	CTCAGCTTCC	CAAGTAGCTG	GGATTACAGG
47251	TGTGCACTAC	CACACCCAGC	TAATTTTGTA	TATTTAGTAG	AGACAGGGTT
47301	TTACCATGTT	AGCCAGGCTG	ATCTCGAACT	CTCGACTTCT	GGTGATCCAC
47351	CTGCCTCAGC	CTCCCAAAGT	GCTGAGATTA	CAGGCGTGAG	CCACCGTGCC
47401	CGGCCCTTTG	CCCCTGTTTT	AATGGGGTTG	TCTTCTTGCT	ATTGAGTTCC
47451	TTATATATTT	TTTATATTAA	CCCCTTATCA	AATGTATGGC	TTGCAAATAT
47501	TTTCTCCCAT	CGTAGGTTGT	CTCTTCACTC	TAATGATTGT	TTCCTTTGCT
47551	CTGAAGACAC	TTTTTAGTTT	TATTTATTCC	CATTTGTCTA	TTTTCACATT
47601	TGTTGCCTAT	AAGCAGGTTA	GAAAATTATA	CAGATTATAA	ATAGTTCCTG
47651	AATTTGTGTT	TTACTAAACG	TAGCCTACAC	AGATGAAAAC	AGGAAAGCTA
47701	CACTTCAGAA	TCTGTGATAT	TTGATGTCAG	AAGTGCATCC	CTGAAAGCAA
47751	TGGGTCCATT	CTAAATCTCC	TAACCTCTAA	CCATAATTG	TTCTATATTT
47801	ATCCTGAGAT	CTCACTCTTA	GGAATAAAAA	CACATTGAGA	AGTCCTGAGT
47851	CTCTATTTTA	CTATTTTCT	GAAGTGCCTG	TAGTGTGTGT	GTTTACATCT
47901	AAATAATAGC	TGTCACCACT	TTCTGATCAA	TTTTAAAAAC	TAATTTTAAA
47951	TAAGTGTTTT	TCATAAATAA	TCCTGGATTT	AGTTCTAAAA	TCAGAATAAA
48001	CTATGCAAAC	TTTGAATCCA	TTAATCAAAA	TGCTTTTAGT	TTCCATTCCA
48051	ACAAAGGCAG	ATAAACAGCC	CCTTCAGACC	ACTGTGGTTT	GAAACATAGC
48101	ACTCACTGGC	TGCCTTTTAA	GAGCCTTCAG	GGAGGGAGCA	AAACAACAAT
48151	TTTTGGTTTT	CAGTTTCCCA	GACAGTGAAG	GAGAGATTTA	GTAATTTTCT
48201	CAAGTGAAAA	AGAATTCAAT	AACTTGCAAA	TAGAACTGA	GATCAAATTT
48251	CCAAATAAAG	TATATTGAAT	TTTTGTTTTA	ACTTTTAAAA	TCTCAAGCTT
48301	AAAGCTTTGA	ACATAAGATT	AAAAAAACTT	TTTTTAGTAT	CCATTTTGTT
48351	GGCTTTAGTT	AAATATCATA	CAAAGTAACC	AACCATCTGG	TAACTTTCAC
48401	CTTAGAGAAA	ACATGATAGT	GGTTGTCACC	TATTTCTTCT	ATTGTTTTCT
48451	CTTCATTATC	TTTGCTTTCT	TTTCACTGCA	CTTTGCCAGC	CAACAGAGGA
48501	TGTATGGGTA	CATGTGACTC	ACACCCACTT	GTTTACACAT	GCATCTGTGC
48551	AAATACATAA	GATGGTAGGT	TAAAAAAAGA	AGAATTAGTT	TCTTGTCCCC
48601	TGGCCTTCTC	CCACAAAAGA	AGAATTAGTC	CAGTTGGTTT	TTCAAATATG
48651	ATTCCAGGAT	TCTTAGTGTT	CCCTCGGGCT	CAGGGTGGTT	GATAGGAAAA
48701	GCCTATAATC	CTCTCAGTCA	CTTTTCAGTT	TGTTTAGGGA	ATGGATCAAA
48751	GAAGGAAGAT	TTTACTGGGT	GGCATGATTT	TTTTATTATA	TGAGGGAAAA
48801	TAGCACTTCA	CTGTCTTTTG	TTTAAAGACA	AGCTTAACAG	ATGCTAAAAA
48851	GTACATCTCT	CAGCCAGATT	CCTAGTCAAC	AAGCTGATAG	ACACTAAGAT
48901	TCTGGATTCT	TCATTGATTA	TATTCAGTCA	TTGTTGGGCA	ATTGACTCCC
48951	TGCCATAATA	ATTGGGCCAG	TATCTATAAC	CAGCATTTTA	CAGATGGATT
49001	CGCTAGACTC	TTTCTGTAAG	AGATGTTTCT	AAAAAGAGTT	ATAGTGAGAT
49051	ATGCTTCTAA	GAAAAGTTAT	ACTGTAGTAG	TGTAATGAAA	GCTACTAGTG
49101	TTTTATTAGT	ATTTCAACAAG	AACAATGTTA	CTCTGTCTCC	CATATATAAC
49151	TGTCTATGGG	CTTTTATGAT	TATTCITTTA	AAAAAAAAAA	TACTAAGGTA
49201	ATGCCTACCG	GGGAACTCAT	GGTGCTGGCT	TCATCCAAAG	TCTGAGCTGT
49251	TTTGGCTTTA	TACTCCGAAA	GACTTTATTT	TCATACATCT	TAACATAAAA
49301	CTGGGGCTTT	AAATTGGTCA	TTCAAGGCCA	GGCGCGGTTG	CTCATGCCTG
49351	AAATCCCAGC	ACTTTGGGAG	GCCGAGGTGG	GCAGATCACG	AGGTCAGGAG
49401	ATTGAGACCA	TCCTGGCCAA	CACGGTGAAA	CCCCGTCTCT	ACTAAAAATA
49451	CAACAACAAC	AACAACAAAA	ATAGCCAGGC	GTGGTGGCTT	GCATCTGTAA

FIGURE 3R

49501	TCCCAGCTAC	TCAGGAGGCT	GAGGCAGGAG	AATGGTGTGA	ACCTGGGAGG
49551	CAGAGCTTGC	AGTGAGCCGA	GATCGCATCA	CTGCACTCCA	GCCTGGGCGA
49601	CAGAGCGAGA	CTCCGTCTCA	AAAAAAAAAA	ACATCGGTAA	TTCAAAGCAT
49651	AGACCAGCCC	TTTTTCAAGT	GATGTTGTTC	CCATGACAAT	CCATCAGTGA
49701	AAAACCAAAT	ACCATATTCC	AAGCTGCTAG	TCACAGAGAA	AACAAGCAGA
49751	TGAGATGAAT	GTAATAGAAA	AGACTAGAGT	TAGTTTTGGG	GTCATCTTTA
49801	GCCAACATTG	CATTGCCTGA	AGCTCAGTAA	TCTGAATCCT	TTTTAATTTG
49851	AGCACATCAG	GGAACAGCTG	AATACCCATG	CTGAGGCATA	ATTTAAGCTG
49901	TCAAGTGTCT	CCTGTCAATA	TACATGTGGT	CATCTGATGC	AAGGCAAAGA
49951	GACAGTCACT	CCTGCTTCTT	TATATCCCTA	GCTCCCAACA	TGGTGTCTTA
50001	ATGCATGATA	ATCATGCAGT	AAATGTTTCA	TGATGAGAAC	ATGACTTTGA
50051	GCAAGGCTGT	ATGATCTGCC	TCAGAACAAG	TGAGTCAGTA	AGAATGCAGG
50101	CCCCGGACCA	TAGGAATGTA	TTACAGTTTT	GCCCAAGAAA	CCACAAACGT
50151	TGGAAACACT	CAAGTTTCTT	TCTCGTATAC	ATCAGCTGGT	GTCATGCAAT
50201	GGGACATACC	ATCTGACGCT	TCCCTGTTCT	TCCCTGATTT	GTCCTGCATG
50251	TCTCCAATAC	CTCTTTCCAA	CCACCTCATC	TCCCCACCTC	ACCTTTCTTT
50301	TTCTTTGTTT	GGCTTTATAT	AGGTGCTGGG	AGTCCCTACA	GAGGATACTT
50351	GGCCGGGAGT	CTCCAAGCTA	CCTAACTACA	ATCCAGGTAA	TATTGCTCTG
50401	AGCTTCTGAA	TACTCTGAGA	ATTAGTAATG	TAAGGAGAGC	ATTGGCCACG
50451	CTAACAGGGC	GTTCTTGTAT	TGTGAACTCA	GCGGCAAAGA	TGGGTGTAGA
50501	GGAATTTCTA	CATTATATA	TTCCCTGACT	AATCTTTGTA	TGAGGAAGAC
50551	ACTGAAAGAG	TAGCTGAGGT	TAGACCAGTT	CCCCAGCTCT	GTAACACACA
50601	AGTAGCAAGC	TGAATAGAAT	TTGAAATGAC	TATTACTGTG	GATTCCACAT
50651	CCATTGTCAA	ATACCCAATG	GCTCAAAAGA	ACAACCTCAA	AGATGGGCTC
50701	ACTTTTGGGC	CCCCTGACTG	TCATAAGTGT	ATTGATTAGT	ATTGAATTGC
50751	ATATGTATAA	AAAGAAAAGCT	AATGCAACAG	AACAGAGGTA	GAGGCTCGCT
50801	AGGCCTAGGA	CATGCCAAGT	AAGCTGTCTG	TAGGTTATAC	TTACTAAGAG
50851	TTCAATTCATT	GCCTGTAAAC	CTGACACTTG	GTCATTGTCT	CTCACACATT
50901	TCATCTTTTCA	AGACTGGCTT	CTGGGATCGA	TTTAGAAGTG	CTGGAAGTGT
50951	TATCCATGGG	GGAATTCTTT	GAGAAGCTGT	CGCAGGGCCA	CATCAGAGGG
51001	ATCAGATTAA	GCAGTAGTCA	CTTCAAGGAT	GTTGAGACAG	AGGGGAGGAG
51051	ACAGGCACTG	AACTACAGGA	TGAAGGATCA	TATTAGAAGC	TGAAGAAGCA
51101	AATAAAGCCC	ATGCCAAAGC	TGAGCTCTCA	CTGGCAGGGT	TGAAGGGGAG
51151	GTAGAAAGGT	ACAGATAACG	ACAAGATTAG	GGTGGATATG	CTCCAAGCCA
51201	GATTTTTCTA	GTCTTTATGG	TCTTACATTG	TTCCATTACT	AAAAATGAAA
51251	TCTTCCCAAA	TTGTTGTCTT	TACTTTTTTT	TTTTTTTTTT	TGAGATGGAG
51301	TTTTGCTCTT	ATCGCCCAGG	CTGGAGTGCA	GTGGCACGAT	CTCGGCTCAC
51351	TGCAACCTCC	ACCTCCTGGG	TTCAAGCAAT	TCTCCTGCCT	CAGCCTCCCC
51401	AAGTAGCTGG	GACTACAGGC	ACCCGCCACC	ATGCCCAGCT	AATTTTTTGT
51451	ATTTTTAGTA	GAGATGAGGT	TTCAACCATG	TGGCCAGGCT	GGTCTCGAAC
51501	TCCTGACCTC	AGGTGATCCA	CTTGCTTCAG	CTTCCCAAAA	TGCTGGGATT
51551	ACAGGCATGA	GCCAGCGCGC	CTTGCCTGTT	GTCCTTACTA	ACTTTGGTAT
51601	GAGATTATCC	TGGAAGGGTT	TCCTGAGAGC	AAGAAATTGT	AGGTAGAGTT
51651	AAAATGTGAT	TAAAGAAGAG	AATAAAATAC	ATAGGGAGCT	GGGGACTCTT
51701	TTTCTTATTT	TCTTTAGCAT	CCAATACTTT	TGCTTACAGC	TATCCATAGG
51751	GATCTGGCAT	CTTGAACCAC	CAGGATTATG	GAAGCCCTAC	AGCAAGCTAA
51801	AGACTAACTG	TAAAGTCCTT	TCAGCTGCTT	TGTGAATGGT	TATATCTATT
51851	GCTAAAAGGC	CTTAATATCA	TTTGCAAATA	GTTTATGATT	TCTAACTATT
51901	TTTCTAGAGT	TTAACACGTG	AGAAAAATGC	TACTCTCTGG	TCACAGGACT
51951	TAGAATAGTG	CCTATTTCCA	TTGGTCTGAG	ATAGAGAAAA	AAGAACAAGT
52001	TTCTTGTGGA	GCCGTGGTCC	AGTCTGCAAA	TTGCTCCTAT	CTCCAGTTGC
52051	TATGGTTTCC	AGGAGAACGT	GGCTCTCATC	TTTTCTGCTC	CTGCCTGTAC
52101	TTCTCCCTGT	CCACTCTGTT	CTCATATTTT	CCTCAGCTTC	CTAACTGAGG
52151	ATGCCAGCAG	AAGTTTAGAG	TCACAGATGG	ATTGTAGGAA	ACAATTTGGA
52201	TGATGCCAAT	ACAAAGCTAC	TGTGGTGGGC	ATATGCTGCT	CCCCCAAAC

FIGURE 3S

```
52251 TCAGACATTT GGGTTTCAGG TTGGTCCAGG CAATCAACAG TGATCCTTAA
52301 TACAAAATGT CTTGGTGAGA GCAATAATCA AGAAACTTGG CCAAAGTGCT
52351 TCCCTGCCAG ATTGTGTGCT TAATAAGATA ACTGGGTTCC AATAAAACAG
52401 AGAAAATATG TTACATTTTA AAAAATTTTC TGTTGTTTCA AAACAATGTG
52451 CAGTTTTTCT ATATAAGAAG AAAAGTCTCC AGGCCCAACA TCCATAGGGC
52501 TCATCATCCA TTGTTTTTCT TTAAAGTTTT CAATTTAATC CAAATAAGTC
52551 AAAAATTTTC AGGTACCTAC TATCTGCCAG GTGCTGTGCC GTGCGCTGGG
52601 GCTACACAGA TGGAGAGGGT GCATTCTTGG ATCTCTAGTG TTTGGGTTTG
52651 GATTCATTCA CCCACACTCT TTCACCAGTT CTCTTTGTGA CTGGGGTGCT
52701 CATTTGTGAG CCCTGCTTCC ATGGCTTGGA GAGTTTGTGG CTGTGGGCCA
52751 GGCTGAGCTT ATGGAGCAAA GGGAGTTGGA ACCTTAGCCA TAGACATGAT
52801 GTCTAAACCT GGATTTGGAA ATCTTAAAAG TCCAGCCTAT CTTGGGCCAT
52851 GGGGTCAGTA TTATTGATAA CTCAATCCCA AGGACTGTGT TTTAAAAGGG
52901 TCTCCAACAT CTGCATTTCA GGAACATCCT CTTACGTGAG TCAATAAGTT
52951 CCTTTTGAGC CACCCCCTAC CCATCCCCAT CCCTGAGCTG CTGTGGCTTC
53001 TAAACACTTG AATGTCAGTG ATTAAGGGGA GCAGAAGACA AGCTGGGAGC
53051 CAGGAAAGTG TCACAGATGA GCACCGTGTC AGCAGCATTG TGGATGAGCT
53101 TCCCATTTCCT TTCCTTTTCA TTCTAAGTAG TCCTAGGAGC CCCCAACTT
53151 TGAATCAGCC AGTACAATTT TGAGGGAGTC CAGTTGTCCG GAACTTGGGA
53201 GAACCATCCA GTGTCCATCT ACACCCATGC CTCATTCTCT AGGCCTTATC
53251 TGGACACCTC TAGGAGGACA GCAAAGTTTC CATTTGTACA GCTTTTAAAA
53301 AGTCACCTGA TGCTGACCCA GTCGGATTTC TC (SEQ ID NO:3)
```

FEATURES:

Start: 2118
Exon: 2118-2240
Intron: 2241-2946
Exon: 2947-3096
Intron: 3097-3310
Exon: 3311-3405
Intron: 3406-7938
Exon: 7939-8018
Intron: 8019-18260
Exon: 18261-18355
Intron: 18356-19116
Exon: 19117-19179
Intron: 19180-29296
Exon: 29297-29420
Intron: 29421-31091
Exon: 31092-31212
Intron: 31213-42825
Exon: 42826-42919
Intron: 42920-50322
Exon: 50323-50406
Stop: 50407

CHROMOSOME MAP POSITION:
Chromosome 2

ALLELIC VARIANTS (SNPs):

FIGURE 3T

DNA Position	Major	Minor	Domain
864	C	T	Beyond ORF(5')
2111	C	G	Beyond ORF(5')
3259	C	T	Intron
3673	A	G	Intron
3747	A	G	Intron
3788	T	G	Intron
8034	T	A	Intron
27740	G	C	Intron
27752	C	T	Intron
29927	T	C	Intron
30772	A	G	Intron
36310	T	G	Intron
36327	T	C	Intron
40618	T	C	Intron
40928	T	C	Intron
41044	A	-	Intron
41311	-	G A	Intron
41313	-	A G	Intron
44701	C	A	Intron
46020	T	C	Intron
46036	A	G	Intron
46095	T	A	Intron
47608	T	G	Intron
51949	-	C	Beyond ORF(3')
52150	G	A	Beyond ORF(3')
52426	-	T	Beyond ORF(3')

Additional SNPs 3' of the ORF (DNA positions refer to the genomic sequence provided in U.S. Serial No. 60/265,151, Attorney Docket No.CL001098-PROV, filed January 31, 2001):

56707	-	T
57444	A	G
58021	A	G
58064	A	C
59067	T	C G
60034	A	G
63709	A	T
63817	G	A
64845	A	-
64848	G	-
64914	G	T
67367	G	A
67497	T	A
68252	G	-
68580	C	G
69990	G	A
71472	A	G
71664	T	A
71677	A	G
72590	T	C
72757	G	C
72863	A	C
74565	C	T

FIGURE 3U

74850	A	G
75462	G	C
76045	A	G
79973	G	A
83181	-	T
84935	C	T
87476	C	G

Context:

DNA

Position

864 ATATTCTGAGAACTAGCTTCTCACTCTCTCAGTTGTCAAGTCAAACTTTAATGGTCTTT
GGCCGGGTGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGA
TCACAAGGTTAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCTCGTCTACTAA
AAATACAAAAAATTAGCCGGGTGCGGTGCCAGACGCCTGTAGTCCCAGCTGCTCAGGAGG
CTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGC
[C, T]
ACTGCACTCCAGCCTGGGCGACAGTGCAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAA
GTTGAATGGTCTTTGAGCCAAGTAGTCTTCTTTCTTCTTCTTCTTTTTTTTTTTTTTT
CAAAAAATATCTCTAGATTGAATCTTGGAATTGGCTTAAGTCTTCTCTTGTGGCAATT
TTGAAATGAAAAAATACATGCTCATAATTAAATTACCTGAACATTTTAAAAAACCATCAT
GAGGTTCAAATATCAAATATTATAAATATTGTTGTGATAATAGACATAACTCTATTTT

2111 TACCAATAGCACTAACTTGTGGCCAGAACAAGAACCTTAACTGTGCCAAATTTTATTCTA
TTCAATAACAGCTGCCTCGTTTTAGTGTGTCACATCTGAATGCAAGCAATCCCTGTCTG
ATGTGGAGTTTCTTGCAGTGAAGGAAAACTGCTGAAGTTGTGAGGCTGCTCCAGGCA
GAGCCATCATGTGAGTCATATGAAAGCTCCACGCTGCTGACCTCTGGCAAAAAGGAGAG
AACAAGGATAGGAGAGGCAGTGGGGGAAAGGTTCAAGTGCGGGTTTTCTCCTTGAACCTA
[C, G]
AAGATTATGGGTCAAGAGCTGTGTGCAAGACTGTACAGCCTGGATGCAGCTGCTACCAT
TGTTTCAGAGGGAGGCGAGGCACACAGCTGTGCGAGGAGTCAGCCTGAGACCACGGAGGCT
GCGTTCAAGGTATTTGTATCCCAGGAGAGAGCATCTTCTCTATTGATAAACCAAGGAGT
TCAGACACTCCCTTTTTGTAGCGGGATCTGATTCTTCTGCGGTAGGTCTAAACCAATAAA
ATGAAAATTCTATTAAAGTCACAGAAAATTTATGGCTGTAGTTATCAAATTTGGGGAATT

3259 AAAGAAGCATCATGTTCCATGACTTCATTTACCCCCAGGGGACTTCAAGCTGCCCCGTGCC
CAGAAGTTCAAGAGTAAAAGGCCACGGAGTAACAGTGATTGTTTTAGGAAGAGGATCTG
AGGCAAGGTTTTAGTGGGTGAGTGAGCAGCTGATGTTGATCAAGAAGAAATTAATGTGA
GCTTGTCTACGGAGGCCGCCCTTGTCTCCAGGGCAATTAAGTGAAGCGAGCTTCCCAAGT
CTGCTCTGGCAATGCTGTCTAATTTCCCTGGGGAAAAAAGTCAACACTAAAAAAGTG
[C, T]
TCTTTCTCTTCCCTTTACCCGCTCCTTTTCCCCATTCCCCTAGAGCAGAGGAAGAGC
CTCCCTTTTGGGGCAGCCTCATCTTACTTGAACCTGGAGAAGCTGGGTGAAGGCTCTTAT
GCGACAGTTTACAAGGGGATTAGCAGGTGAGTGACACATAGCTGGGAGAGACTTTAGAGA
TGAGAGTCCCGCCCCCAATTTATATTATAAAGCCAGGTGAGACATCATAGAAGTTCA
TAGCACTCAGGACCTGTGCAAGACACCATGGCCGACAGGGAGAGAGACATGATAACTTAA

3673 CTCTTATGCGACAGTTTACAAGGGGATTAGCAGGTGAGTGACACATAGCTGGGAGAGACT
TTAGAGATGAGAGTCCCGCCCCCAATTTATATTATAAAGCCAGGTGAGACATCATAG
AAGTTATAGCACTCAGGACCTGTGCAAGACACCATGGCCGACAGGGAGAGAGACATGAT
AACTTAAACAGCCTTGAAAGAAAAACAACTGCCCTGCCCTAATTTAAATCAGCCCACT
TAAATGTTTATCAGCCTTCCCTTCTTGCAATCAATTCAGAGAATTCAAAGAAAATAGAC
[A, G]
TTCTCTACTACTGACCCAAAGAACAATTATCACTCTTCAGGCCTGTGGGAGGCACAGTTG
GTAAAGCGTCTTAACAGGTTTTTATATCCCTCCCTAAATCACAATGACAGAGTTTTGT
AATGGCAACTGGAATTTGCTGCTTCAATTCCTCCACCTGGCCTTTATAGAAGAACTGAA
GTTGGTTTCTGCAAAATATGGTACATGCAAAAGATGATAAATCCTAGATTTTTTATATT
GCAAAATACAAAAATGTCTGGAGAATAAAAAACTGCTTATCCAAAAGCTAAGTACTAA

FIGURE 3V

FIGURE 3W

CATTGGTAGAGTAAACTGTAAGTTTCTCTAAATCTAAGTGAATATACAAATTA
TATTGGAATAGATTGAGATTATCCCAAGATGATAAAGAGGTTAACCCACAGATTGTAGCAT
GGACTCCTGT CAGGATGGAGACTCCAGGACACTTGTTCTGTCTCTACCTTCTTTATA
TAAGTGTGAGATGCAAAGTTTTATTCCCATTAAAGTGAAGCAGATTTCTCTAAGTATCA
[T, C]
TGTATCCTTCCATTTTAGCACTTATCGCAGTTTATAATTATATTCACACACATAAATACA
TACATGCATACATACAAATATATATACATGTGTGAGCACACCCCCACACACAAATATATA
TAGATTTGCGTGATGATTTTGTCTCAACTGGACTGTAAGCATAATGAGGGCAGCCTGGGT
TTGTTTTGCTTATCATTTTATCCTTAGTGCCTGGTACCATAGTAGGTGCTTAATAAGTA
CTTGTTGAAAACTGGCTCTATGTGAGCTAAGGAACCACTCTTCTCTGTTTGGCAGATGC

30772 CAGTCCCTACCGTTTATCTACTAACTGGGCTTCTCTGGAGTGCCAAAACGGAAGGTGGC
CATGTTAGTCATGAACAGCTCAGTTTCTGTTACAGAGACCCAAAATTACAGAGGTATAAC
ATGCTAGAAACTTAACTTTCTTTCGCATCACAGTCCTGACCTAAGCAGGCAGAGCATGTA
TGGTGGCCCCATGCTATCTTGGCCCAGGCTGCTTCTGTACGTGGCTCCTCCATCCCCAA
TTGTATGTTTCAAGATGGCTGCCACTTCTGTCTATCACAGCCCAGAGGAGGGAGAAAAAG
[A, G]
GAAGCAGAACCCTTAAACCCCTCCACTAAGGCATAATCTGGAAGTTCACACATCACCTCTG
TTCATATCATATAGGCAAGAAGCTTAGTCACCTGACCACACCCAGCTGCCAAGAAGGCCAC
ATCTAGCTGCAAAGCAGGCCAAAATTTGAGAAATTCATTGATGAAGTGATAGACAAGAG
TCAAGATAGTGATTAGTTCTACTAAAAGCACCTAAAGTTTGTGTGTTATTTTTTCTAATG
GTGTTTACCCTGGTCCAGTGCATCATGGTGCAAGCCAAGGTCCAGAACGATGGGTTTTAT

36310 TAGAGTGTTTTGTTTTGTTTGTGTGTGTAGGCCTGCTGGTGGCAAATTCCTCGTTTTT
GTTTTCAGAAGATAAACCCCTAATTATTGAAAGGTGGTTTTGTTGGGGATGTGATTCTAGA
CTGACAGTTATTTTCTCTCAGAACTTTGAAGATGTCATTCCCCCTTCTTTGTCTTCCATTG
TTGCTGTGAGGAGTTTGCTTTAGCCTTATTATCTTCTTTTGAGGTGATCTCATTTT
CTCTGGATGTTTTAAAGACTTTTTTCTTTCCTTTATGATTATGCAGTTTTCTCTAGGAG
[T, G]
TGTCCAGTGTGGATTTCTTTTTACTTACCCTGTTTGGTATATCTTGTGTTTCTTCCATTT
GTGAATTCATGTCTTTCATCAGCCATTTTCTTTTTGAATATTGACTCTATTCTATTCTCT
CTCTGTAGAGCTCCAATGAAAGACTATTAGACCACATTCTTCTGTTATCCATTTCTCTTC
TCTCCTTCATATTTCCATTTCTTAACTTTCTGTGATGCATTCTGGGTAATTTCTTCAG
CTCATCTACCAGTTCCTTAAGTCTCTCTTAACTATGTATTAGGTTGGTGCAAAAGTAAT

36327 TTTGTGTGTGTAGGCCTGCTGGTGGCAAATTCCTCGTTTTTGTTCAGAAAGATAAAC
CCTAATTATTGAAAGGTGGTTTTGTTGGGGATGTGATTCTAGACTGACAGTTATTTCTC
TCAGAACTTTGAAGATGTCATTCCCCCTTCTTGTCTTCCATTGTTGCTGTGAGGAGTTT
GCTTTTAGCCTTATTATCTTCTTTTGAGGTGATCTCATTTTCTCTGGATGTTTTAAAG
ACTTTTTTCTTGCCTTATGATTATGCAGTTTTCTCTAGGAGTTGTCCAGTGTGGATTT
[T, C]
TTTTTACTTACCCTGTTTGGTATATCTTGTGTTTCTTCCATTTGTGAATTCATGTCTTTC
ATCAGCCATTTTCTTTTTGAATATTGACTCTATTCTATTCTCTCTCTGTAGAGCTCCAAT
GAAAGACTATTAGACCACATTCTTCTGTTATCCATTTCTTCTCTCTCCTTCATATTTTCC
ATTTCTTAACTTTCTGTGATGCATTCTGGGTAATTTCTTCAGCTCATCTACCAGTTCTT
TAAGTCTCTCTTAACTATGTATTAGGTTGGTGCAAAAGTAATTGCAGTTTTTGCCATTA

40618 CCGGGTGTGGTGGCTCACACCTGTAATTCAGCACTTTGGAAGGCTGAGGCAGGCGGATC
AATTGAGGCCAAGAGTTTGAGACCAGCCTGGCGAACATGGTGAAACCCTGTCTGTACTAA
AAATACAAAAATTAGCCAGGCATGCTGGTGCATGCCTGTAATCCAGTTACTCAGGAGGC
TGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACC
ACTGCACTCCAGCCTGAGTGACAGAGTGAGACCCTGTCTCAAAAAAAAAAGAAAAAAAAAA
[T, C]
TGGCAATAAAAAACAACCTGTTGCTTGGTGGAGGAAAAACCTGCTTGCAAAGCTCAGTCTG
ATATCATTTTTTAAACAAAACCTAAGAACAAGCCAGTCAGTTAAGCTAAAACCAAATAT
TTGATTATGAAAAGGGTTTTTGTATATTTTACAGGATAAGATACAAATAAATTTTCAGTC
TTTCTTTTAAATATGATTTCTGTTCCCAAACAGACACAAAGCAATTTTTTAACTTGATC
GTCAAGAAATCTGTTTTCTCTACACAATCAATGAAAAGTAATCTAAACAGTGTTTTGTCA

40928 AAACAACCTGTTGCTTGTGAGGAAAAACCTGCTTGCAAAGCTCAGTCTGATATCATTT
TTTAAACAAAACCTAAGAACAAGCCAGTCAGTTAAGCTAAAACCAAATATTTGATTATG

FIGURE 3X

AAAAGGGTTTTTGTATATTTTACAGGATAAGATACAAATAAAATTCAGTCTTTCCTTTA
ATATGTATTTCTGTTCCCAAACAGACACAAAGCAATTTTTAAACTTGATCGTCAAGAAA
TCTGTTTTCTCCTACACAATCAATGAAAAGTAATCTAAACAGTGTTTGTGAGGCCAGGCA
[T,C]
AGTGGCTCACATCTGTAGTCCTAGCATTTTGGGAGGCCTAGGCAGGTAGATTGCTTGAGC
CCAGAATTTCAAGACCAGCCTGGACAACATGGCGAAACCCCATCTGTATTA
AAAAAAAAAAGACCATATGTCTGCAGTCAGATGGAAAAAGTAAAAATATGTAATAAACACA
TATGAATAATATTAAGGACCATATTTTAAAAATAAACTTGATAATAAATTTTTAATAATAT
TATCTACGATAAAATGTTTTACTTAAATTCGTTCTTTATCATGCCACACAAAAATGGCA

41044
TATGAAAAGGGTTTTTGTATATTTTACAGGATAAGATACAAATAAAATTTTCAGTCTTTCT
TTTAATATGTATTTCTGTTCCCAAACAGACACAAAGCAATTTTTAAACTTGATCGTCAA
GAAATCTGTTTTCTCCTACACAATCAATGAAAAGTAATCTAAACAGTGTTTGTCAGGCCA
GGCACAGTGGCTCACATCTGTAGTCTAGCATTTTGGGAGGCCTAGGCAGGTAGATTGCT
TGAGCCCAGAATTTCAAGACCAGCCTGGACAACATGGCGAAACCCCATCTGTATTAAAAA
[A, -]
AAAAAAAAAAAAAGACCATATGTCTGCAGTCAGATGGAAAAAGTAAAAATATGTAATAAA
CACATATGAATAATATTAAGGACCATATTTTAAAAATAAACTTGATAATAAAATTTTTAATA
ATATTATCTACGATAAAATGTTTTACTTAAATTTGTTCTTTATCATGCCACACAAAAAT
GGCAAAATGATTAAGAGAGTTTTGCAAAATTATGTGGTATAGTGAAAGAGGTTTGGCGTTA
AAAAAAAAAAAAAGAGAGAGAGAGAGAGAAGTATGGGGCCATGGGGATAGTCTCTGTAATCA

41311 GACAACATGGCGAAACCCCATCTGTATTAATAAAAAAAAAAAAAAAAAAGACCATATGTCTG
CAGTCAGATGGAAAAAGTAAAAATATGTAATAAACACATATGAATAATATTAAGGACCAT
ATTTTAAATAAACTTGATAATAATTTTTAATAATATTATCTACGATAAAATGTTTTAC
TTAAATTTCTGTTCTTTATCATGCCACACAAAAATGGCAAAATGATTAAGAGAGTTTGCAA
AATTATGTGGTATAGTGAAAGAGGTTTGCGGTTAAAAAAAAAAAAAGAGAGAGAGAGAGAG
[- , G, A]
AGTAGTGGGGCCATGGGGATAGTCTCTGTAATCAGTCACCTGAACCACTTTTAATACTCAA
AAGACTTATGAGAATAAAAAATCTGATTTTTGCTAAGATTATTAGCAAAATAAATCTTAC
TCCTTCCTGTCCCTCTCTAATTATCCTTCAGCTTGACCATGTATGAAAGAAAAATTTACAT
TTCACTGTTTAATCTATTTAAAGATGAACATTTCCCATTAATCAGGATGCACCTTATAA
TCAGTAGCATCTAACAAATAAAGTCAGCCAGGCTGCAGTTGTGACTGTAGTTAGAATTGC

41313 CAACATGGCGAAACCCCATCTGTATTAAAAAAAAAAAAAAAAAAGACCATATGTCTGCA
GTCAGATGGAAAAAGTAAAAATATGTAATAAACACATATGAATAATATTAAGGACCATAT
TTTAAAAATAAAGCTTGATAATAAATTTTAAATAATATTATCTACGATAAAATGTTTTACTT
AAATTTCTGTTCTTTATCATGCCACACAAAAATGGCAAAATGATTAAGAGAGTTTGCAAAA
TTATGTGGTATAGTGAAAGAGGTTTGCGTTAAAAAAAAAAAAAGAGAGAGAGAGAGAGAA
[- ,A,G]
TATGGGGCCATGGGGATAGTCTCTGTAATCAGTCACCTGAACCACTTTTAATACTCAAAA
GACTTATGAGAATAAAAAATCTGATTTTGCTAAGATTTATTAGCAAAAATAAATCTTACTC
CTTCTGTCCCTCTCTAATTATCCTTCAGCTTGACCATGTATGAAAGAAAAATTTACATTT
CACTGTTTAATCTATTTAAGATGAACATTTCCCATTAATCAGGATGCACCTTATAATC
AGTAGCATCTAACAATATAAGTCAGCCAGGCTGCAGTTGTGACTGTAGTTAGAAATTGCAC

44701 TCTAAAAACTTTCTTGCAAGACAGAGCAATGCTATCTTCACATTATGTTATTGGGTGCTA
TAACATCATCTAAGCTGGAGACAGCCTACTGTCATAGCTTTGGAGTCCAAAGACCTGGGT
TTGAATTCTAACCATTTTCTAGCTAAATGAACATGGGCAAGTTATGTAGTCCCTCTGAAC
TTTCGTTTCCTTGTCTGTAAAATGGCAACAATGATAATAAGGACTTTCTAATTCTTTATT
GAGAATTCATAAAAACAAATGCATAACAAGCTCCATGCACCATAAATGCTCAATAGATG
[C,A]
TTGCTTTCTTCCTGTCCCATACAAATTGTTGTACAGATGTTTCAATAACCTAACTGCTAG
CAAGTATTACCTGAAATTTAACCCGATTGTTCTCTTCTTCACTTAGCAGTATTATTTCT
TGTCACAATAGAGGAAGCACAATTGCAGTTCTGATGCTGCAATGACCTTTTATACATTT
GAAGAGTTTTTCTGGTCATTTAATCAGGAAACAACACTTACTCCCATATATGAGGCGA
GTAACCTACAAGACTCTACAAGGTCTTGTAAGAAGCTATAAGCCAAGGGGGAAAAAAA

46020 AAATTTCAAATAACATTTTAAATATGACATACTATCTTTGAATGACCACACAATTTAAA
AAGCAATCATTTTACGGTTCCTTAGTGTTAGTTCAGTTAGCACAGCACTTAGAAATCATAGAAT
AAAGTGAGCAAGATGCTTCTCAAAGCCTGATCACTCTTAGGACTCACAAATGGGCTAGGT

FIGURE 3Y

ACTATGCTGGAAAGAGAAAAATAATAATTTTCTAACCTGCTTGAGACATAGTGGTATAA
ATGATAACACAGCTGCTGAACGTGATGACTTTCTCACTTTGTCCGCAGAGCAAGAACTA
[T, C]
AGATGCAGTAACAAACTGCATTCAATGAACATGGGACTGTAGATAACAACTAACTTCA
TTTCTTTGGGTACATGCCCTGTATTGGGATTGCTGGATCATATGGTAGTTCCATTTTTAA
TATTTTGAGGAACCTCCATACCATCTTCCATAATGGCTGTGCTATTTGCATGCCACCAT
CAGTGTGCAAATGCTCCCTTTCTCCACATTCTTGCCAACACCTCTTTCATCTTTTGAT
AATAGTTATGAGGCAATATCTCACCATGGTCTAGACTTCATTTGTCTGATGACTAATGA

46036 TTTAAAATATGACATACTATCTTTGAATGACCACACAATTTAAAAAGCAATCATTTTACG
GTTCTTTAGTGTTTCACTTAGCACAGCACTTAGAAATCATAGAATAAAGTGAGCAAGATGC
TTCTCAAAGCCTGATCACTCTTTAGGACTCACAATGGGCTAGGTACTATGCTGGAAAGAG
AAAAAATAATAATTTTCTAACCTGCTTGAGACATAGTGGTATAAATGATAACACAGCTGC
TGAACGTGATGACTTTCTCACTTTGTCCGCAGAGCAAGAACTATAGATGCAGTAACAAA
[A, G]
CTGCATTCAATGAACATGGGACTGTAGATAACAACTAACTTCATTTCTTTGGGTACATG
CCCTGTATTGGGATTGCTGGATCATATGGTAGTTCCATTTTAAATATTTTGAGGAACCTC
CATACCATCTTCCATAATGGCTGTGCTATTTGCATGCCACCATCAGTGTGCAAATGCTC
CCTTTCTCCACATTCTTGCCAACACCTCTTTCATCTTTTGATAATAGTTATGAGGCAA
TATCTCACCATGGTCTAGACTTCATTTGTCTGATGACTAATGATATTGAGCATTTTTTC

46095 GGTTCTTTAGTGTTTCACTTAGCACAGCACTTAGAAATCATAGAATAAAGTGAGCAAGATG
CTTCTCAAAGCCTGATCACTCTTTAGGACTCACAATGGGCTAGGTACTATGCTGGAAAGA
GAAAAAATAATAATTTTCTAACCTGCTTGAGACATAGTGGTATAAATGATAACACAGCTG
CTGAACGTGATGACTTTCTCACTTTGTCCGCAGAGCAAGAACTATAGATGCAGTAACAA
AACTGCATTCAATGAACATGGGACTGTAGATAACAACTAACTTCATTTCTTTGGGTACA
[T, A]
GCCCTGTATTGGGATTGCTGGATCATATGGTAGTTCCATTTTAAATATTTTGAGGAACCT
CCATACCATCTTCCATAATGGCTGTGCTATTTGCATGCCACCATCAGTGTGCAAATGCT
CCCTTTCTCCACATTCTTGCCAACACCTCTTTCATCTTTTGATAATAGTTATGAGGCA
ATATCTCACCATGGTCTAGACTTCATTTGTCTGATGACTAATGATATTGAGCATTTTTTC
CATATATCTCTTGGCCATTTGTAGGTCATCTTTTGAGAAATGTGTATTGAGGTTCTTAGT

47608 GTTAGCCAGGCTGATCTCGAACTCTCGACTTCTGGTGATCCACCTGCCTCAGCCTCCCAA
AGTGCTGAGATTACAGGCGTGAGCCACCGTGCCCGGCCCTTTGCCCACTGTTTAAATGGGG
TTGTCTTTCTGCTATTGAGTTCCTTATATATTTTTTATATTAACCCCTTATCAAATGTAT
GGCTTGCAAATATTTTCTCCCATCGTAGGTTGTCTCTTCACTCTAATGATTGTTTCCTTT
GCTCTGAAGACACTTTTTAGTTTTATTTATTTCCATTTGTCTATTTTCACATTTGTTGCC
[T, G]
ATAAGCAGGTTAGAAAATTATACAGATTATAAATAGTTCCTGAATTTGTGTTTTACTAAA
CGTAGCCTACACAGATGAAAAAGGAAAGCTACACTTCAGAACTGTGATATTTGATGTC
AGAAGTGCATCCCTGAAAGCAATGGGTCCATTCTAAATCTCCTAACCTCTAACCATAAAT
TGTTCTATATTTATCCTGAGATCTCACTCTTAGGAATAAAAAACATTTGAGAAGTCCTGA
GTCTCTATTTTACTATTTTCTGAAGTGCTGTAGTGTGTGTGTTTACATCTAAATAATA

51949 TTAAATGTGATTAAAGAAGAGAATAAAATACATAGGGAGCTGGGGACTCTTTTTCTTAT
TTTCTTTAGCATCCAATACTTTTGCTTACAGCTATCCATAGGGATCTGGCATCTTGAACC
ACCAGGATTATGGAAGCCCTACAGCAAGCTAAAGACTAACTGTAAAGTCCTTTCAGCTGC
TTTGTGAATGGTTATATCTATTGCTAAAAGGCCTTAATATCATTTGCAAATAGTTTATGA
TTTCTAACTATTTTTCTAGAGTTTAAACAGTGAGAAAAATGCTACTCTCTGGTCACAGGA
[-, C]
TTAGAATAGTGCCTATTTCCATTGGTCTGAGATAGAGAAAAAAGAACAAAGTTTCTTGTTG
AGCCGTGGTCCAGTCTGCAAATTGCTCCTATCTCCAGTTGCCATGGTTTCCAGGAGAACG
TGGCTCTCATTTTTCTGCCCTGCCCTGTACTTCTCCCTGTCCACTCTGTTCTCTATTTT
CCCTCAGCTTCTAACTGAGGATGCCAGCAGAAAGTTTAGAGTCAAGATGGATTGTAGGA
AACAAATTTGGATGATGCCAATACAAAGCTACTGTGGTGGGCATATGCTGCTCCCCCAAAC

52150 TGCTAAAAGGCCTTAATATCATTTGCAAATAGTTTATGATTTCTAACTATTTTTCTAGAG
TTTAAACAGTGAGAAAAATGCTACTCTCTGGTCACAGGACTTAGAATAGTGCCTATTTCC
ATTGGTCTGAGATAGAGAAAAAAGAACAAAGTTTCTTGTTGGAGCCGTGGTCCAGTCTGCAA
ATTGCTCCTATCTCCAGTTGCCATGGTTTCCAGGAGAACGTGGCTCTCATCTTTCTCTGC

FIGURE 3Z

CCTGCCTGTACTTCTCCCTGTCCACTCTGTTCTCTATTTTCCCTCAGCTTCCTAACTGAG
[G,A]
ATGCCAGCAGAAGTTTAGAGTCACAGATGGATTGTAGGAAACAATTTGGATGATGCCAAT
ACAAAGCTACTGTGGTGGGCATATGCTGCTCCCCAACTTCAGACATTTGGGTTTCAGG
TTGGTCCAGGCAATCAACAGTGATCCTTAATACAAAATGTCTTGGTGAGAGCAATAATCA
AGAACTTGGCCAAAGTGCTTCCCTGCCAGATTGTGTGCTTAATAAGATAACTGGGTTCC
AATAAACAGAGAAAATATGTTACATTTTAAAAAATTTCTGTTGTTTCAAAACAATGTG

52426 TTTTCCCTCAGCTTCCTAACTGAGGATGCCAGCAGAAGTTTAGAGTCACAGATGGATTGT
AGGAAACAATTTGGATGATGCCAATACAAAGCTACTGTGGTGGGCATATGCTGCTCCCC
AACTTCAGACATTTGGGTTTCAGGTTGGTCCAGGCAATCAACAGTGATCCTTAATACAA
AATGTCTTGGTGAGAGCAATAATCAAGAACTTGGCCAAAGTGCTTCCCTGCCAGATTGT
GTGCTTAATAAGATAACTGGGTTCCAATAAACAGAGAAAATATGTTACATTTTAAAAAA
[-,T]
TTTCTGTTGTTTCAAAACAATGTGCAGTTTTTCTATATAAGAAGAAAAGTCTCCAGGCCC
AACATCCATAGGGCTCATCATCCATTGTTTTCTTTTAAGTTTTCAATTTAATCCAAATA
AGTCAAAAATTTTTCAGGTACCTACTATCTGCCAGGTGCTGTGCCGTGCGCTGGGGCTACA
CAGATGGAGAGGGTGCAATCTTGGATCTCTAGTGTTTGGGTTTGGATTCAATCACCCACA
CTCTTTCACCAAGTTCTCTTGTACTGGGGTGCTCATTTGTGAGCCCTGCTTCCATGGCT

Additional SNPs 3' of the ORF (DNA positions refer to the genomic
sequence provided in U.S. Serial No. 60/265,151, Attorney Docket
No. CL001098-PROV, filed January 31, 2001):

56707 CTGCCAAGATCGATGCTGGGTGGAGTAGCCCGATTCTACAGATGAGGAAACAGAGGCTTT
CTCCTAGGCTCACAGAGAGGTGTATACTTATTGGAAATGGCTGAAATCTGCATCCAAACC
TTGTTCTCCTTTCATTAAATCATGTTGTATCCCTCTGTCTCATTTTGCAGGATGAGTCTGA
AAAATAAATTATATTGAATTGCATCTGCTATAGTGCCTAACTTTAGTAGGTACTCAATA
AAAGTTCCCATTCAGTTTTTTTTGTTGGTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
[-,T]
TTTAGATGAAGTCTCACTTGTACCCAGGCTGGAGTGCACTGGCATGATCTCGGCTCACC
GCAGCCTCCGCTCCTGGGTATAAGCGGTTCTCCTGCTTCAGCCTCCCGAGTAGGTGGGA
ATACAGGCGCACGCCACTGAACCCAGCTAATTTTTGTATTTTATAGTAGAGACAGGGTTTC
CCCACAGGGCTTTCCCTGGGAGAATCCTTGTGCATCTACATGCTACATAATGGGTATCCA
GTAAGGGCTACTAAATCACAGACAACATTAGTGTTACCATTGTTAATTTTCAACCAACAT
[A,G]
GTATAGTGGAAGAGTGCTGAAGTTTTCTACAGAGCACACCTGACCACTTCTAGTGCTTC
TAGTATTTTACACAAGCCCCCTACCTGGCACATAATAAGTAGTCAGTAGATATTTGTGAA
ATGAAATCAATGACTAAGAGTTAGAAAACCTGAGTTCTAGTTCCAATTGCACCTCTTGG
ACTCTAAATAATTCTTATTGTCTGCTTTGCAAAGAAGAACATGTAAGTTATTATTACCT
TAATAATGGTAATAATAATTGAGGACTAACTATGAGCTAGACACTTTACATATTTTACTT

57444 CTTTTGTTTTTACTTGCATGGCCTAAACCTTGCTGAATCCGCACATCCTAAGAGCTGAC
TCTGAGTTTTCAAATGCCTACCTAAGTCAGTTGTGTGCCCGTTAAGGCTGTTCTTATTTG
GTGATGGGTCCATTCTGCTCCCCACACCTAGACTGCAGTAATATGTCTGCCCACTCTGTA
CCCACAGGGCTTTCCCTGGGAGAATCCTTGTGCATCTACATGCTACATAATGGGTATCCA
GTAAGGGCTACTAAATCACAGACAACATTAGTGTTACCATTGTTAATTTTCAACCAACAT
[A,G]
GTATAGTGGAAGAGTGCTGAAGTTTTCTACAGAGCACACCTGACCACTTCTAGTGCTTC
TAGTATTTTACACAAGCCCCCTACCTGGCACATAATAAGTAGTCAGTAGATATTTGTGAA
ATGAAATCAATGACTAAGAGTTAGAAAACCTGAGTTCTAGTTCCAATTGCACCTCTTGG
ACTCTAAATAATTCTTATTGTCTGCTTTGCAAAGAAGAACATGTAAGTTATTATTACCT
TAATAATGGTAATAATAATTGAGGACTAACTATGAGCTAGACACTTTACATATTTTACTT

58021 CTAGACACTTTACATATTTTACTTTACTTTGATTCACAACAGCCTTATCAGATAGAGACA
ATGTTGTAAACCTACTTTACTGATGAGAGAGCTGAGGCTTTGAGAGAGGTATGTGACTT
GCTTAGGGTCACCTAACAGGAAGGGGTGACCTAGAATATCCACACCTGTTGGACTCCA
AGTGGGTCTAGCCGATTCCACTTTACCTTAATTATCAAAGGGCAGATATAATGATTG
GTAATTAACACAGTGCCCTAGACTGGGGACTGGCCATAAACTTTTGCAGGTTTCATTCCA
[A,G]
ATGATTATGTCTTTCCACCCAGACGTGATTTTAGAATCTGTGAGCCTGGCGACATATTT
AGGAGTGTAATCTGAGTGGAGTTTCTACCCTGGGACTCCAGCAGCCTCCCTCGCTACAGC
TAATGAAGCCACTGGCGTTCACTGAATCTGAACCTCGATTGGGCTCATTACTGTCTCA
CTTCTGGAGCGCTGCTGAAAGCTCCTGGGAGTTACTATTAAACATCTTTATTAAACCGTC
CCCCAATCAGTCAGTGAAATTAATTTAGATACACAGCCACTTTGATCTTCATTAATGGT

58064 CTTATCAGATAGAGACAATGTTGTAAACCTACTTTACTGATGAGAGAGCTGAGGCTTTG

FIGURE 3AA

AGAGAGGTATGTGACTTGCTTAGGGTCACCTAACCAGGAAGGGGGTGACCTAGAATATCC
ACACCTGTTGGACTCCAAGTGGGTCGTAGCCGTATTCCACTTTACCTTAATTATCAAAGG
GCAGATATAATGATTTGGTAATTAACACAGTGCCTAGACTGGGGACTGGCCATAAACTT
TTGCAGGTTCAATTCCAAATGATTATGTCTTCCACCCAGACGTGATTTTAGAATCTGTG
[A, C]
GCCTGGCGACATATTTCAGGAGTGTAATCTGAGTGGAGTTCCTACCCTGGGACTCCAGCA
GCCTCCCTCGCTACAGCTAATGAAGCCACTGGCGTTCAGTGAATCTATGAACCTCGATTG
GGCTCATTACTGTCTCACTTCTGGAGCGCTGCTGAAAGCTCCTGGGGAGTTACTATTAAC
ATCTTTATTAACCCGTCCCCAAATCAGTCAGTGAATTAATTTAGATACACAGCCACTT
TGATCTTCATTAATGGTTGCTTCTAGTTTCTACATTTATTTTTAGTTTTCTCATCTTTAA

59067 CTGTAATCCCACCACTTTGGGAGGCCGAGGCGGGTGGTTCAGTTGAGATCAGGAGTTCGA
GATCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCAGG
TGTGGTGGCAGGCACCTGTAATCCCAGCTACTCAGGAGACTGAGGCAGGAGAATCACTTG
AACCCAGGAGGCAGAGGCTGCAGTGAGCCAAGATCATGCCGCTGCACTCTAGCCTGGGCA
ACAGAGTGAGATTCATCTCAGAAAAACAACAACAACAACAAAGAAACACACATAAAACA
[T, C, G]
AGCAGGTATACAAGTGGGCTCACCTGAGTTACTTTAACGTTTTTAAAGTAAGGTTTAATA
TATTTATTTCATTTTATTTTTCATCCAACCATCTACTTCTTATTTATTGAGCAAAATATG
TATTGAATGCTAGGTACTAGGGACTGAGAGAGTAAAAAATAAATATGACACTGGTACCTG
CCTTCCAGGAATATAGTCTAGAGGGGAAAAATAAATAAATAACAATGTGGAAAGTATAC
TACAGCAGCATTGCCTGGGGATCTTTAAGAAACGAGGGAAATCTTGACTTGGCTGTGAT

60034 AGCCACCGTGCTGCCCTAGGGATGGTTTTTAAAGAAAGAGATGTGAGCTTGGCCTCCCA
AAGTGCCGGGATTACAGGCATGAGCCACTGTGCCCGGCCACCCCTGCTATTTTATTCAAA
GGAAACAGAAGGGGGAAGGAACAGATTTATAGAGAAGGTAATGAGTATAAGGTTTTAACA
TTTTGAGATTAAGGTATCTGTGGAACCAAAAATGGAGATATCTAAAAAGCAAGTAGAAA
TATAAAGTGTGAGTACAAAAGTCCAGCCTAGAAATACAGAAAGTCACATGCTTAAATCGGT
[A, G]
TTTTAAAGCCTCAGGTGTGAATTTAGTTGCCCAAAGGAGAGAGTGTAGAGAAAAGAAGAAAG
GACAATGAGGGAACCCCTGTGGGGCCAGTACTGCAGGACTGGGTAGAGGGAAGGGAGTCTT
TAGAAGCTGAGAAGGAACAGCCAGAGGAGCTAAAGGAGACTAGTAGGTAATCCTAGCAAT
ACCATGGAAATCATATGGCCAGCACTCACTGGAAGAGGGCTGGGTTCCATGCCTGTGTAT
TCTCAATGCTGAGCTCATTGGCTGCATGTGGTGGCCCTTCAATATTTGTGGAGACTACAA

63709 TACTTTACAACCCTATGCAGTAGAACTATTACTATCCCTCTTCTGCAGGTGGGAAAAC
TGAGGCCAGTGAGGTTAAGCAATATCTTCCGGTCACACAGCTGGTAAGAGGCATAGTGT
GGGTTCAACCGGGTCTGGGTCCAAGTGCTGGCCACGCATTGTTTATACTGCCCATAAAC
TTTTCAAAGGAAGGGAAAGAGGAAGGAAAAGCAGATAGGATTTATTTTGTAAATGGTCC
AGAGCAGGCATTTTGCCTCATTATTTTATTGGTTTCGCTTCAGGTGAATACCACCTTCAA
[A, T]
TTGCATTGAGAAAACTGAGGGTTGCCCTACAGAATGCGAGAAAAATTTTTGCAATCTACT
CATCTGACAAAGGGCTAATATCCAGAATCTACAAAGAACTTAAATAAGTTTACAAAAAAA
AAAAACCATCAAAAAGTAGGCAAGGATATGAACAGACACTTCTCAAAAGAAAGACATTTA
TGCAGCCAACAGACACATGAAAAAATGTTTCATCATCACTGGTCATCAGAGAAATGCAAT
CAAAACCACAATGAGATACCATCTCCACCAGTTAGAATGGCAATCATTAAAAAGTCAGG

63817 GAGGCATAGTGTGGGTTCAACCGGGTCTGGGTCCAAGTGCTGGCCACGCATTGTTTAT
ACTGCCCATAACTTTTCAAAGGAAGGGAAAGAGGAAGGAAAGCAGATAGGATTTATTTT
GTTTAAATGGTCCAGAGCAGGCATTTTGCCTCATTATTTTATTGGTTTCGCTTCAGGTGAA
TACCACCTTCAAATTGCATTGAGAAAACTGAGGGTTGCCCTACAGAATGCGAGAAAAAT
TTTGCAATCTACTCATCTGACAAAGGGCTAATATCCAGAATCTACAAAGAACTTAAATAA
[G, A]
TTTACAAAAAATAAACCATCAAAAAGTAGGCAAGGATATGAACAGACACTTCTCAAA
AGAAGACATTTATGCAGCCAACAGACACATGAAAAAATGTTTCATCATCACTGGTCATCAG
AGAAATGCAAAATCAAAACCACAATGAGATACCATCTCCACCAGTTAGAATGGCAATCAT
TAAAAAGTCAGGAAACAACAATGCTGGAGAGGATGTGGAGAAAATAGGAATGCTTATACA
CTGTTGGTGGGAGTGTAACCTAGTTCAACCATTTGTGGAAGACAGTGTGGCGATTCTCTCAA

64845 TAGGAGAAATAGCTAATGTAAATGATGAGTTAATGGGTGCAGCAAACCAACATGGCGCAT
GTATACCTGTGTAACAAACCTGCAGGTTGTGCACCTGTACCCTAGAACTTAAAGTACAAT

FIGURE 3BB

AATGAAAAAATTAATTAATAAATCAGAAAAAAGAAAGAAAACTGAGGGTTGCCA
TGGATGGTCAAAGTATCTTACATGAGGTCTCAGCAAACTGAAGCAGCAGAGTCTGTATT
GAAACCCTAAGTCAGCTAACCCCAACCCACGTGCCACAAGAACCCCACTCAAGTTAGAA
[A, -]
GAGTATTAATTAATTTGGAGGCCAAAAACACAGCACATAGACCTCTCAGAAGGGAAAAATA
GAAAATGGGAAAGGATGGAAATGGATTTTCATTTTGTTGATTGAAATTGGGAGATGACTGA
ATGAGGAAATATTTTGAATTTTGTGGCCAGGGAAGAGCTGTAAATAGGCAGCAGAAAAGT
GGTTTGAAGAGAAACATACTAAACAAATGCCAGATATTCTTATCTTTACTGGTTATTTTG
AACTTAGGCAAAATCATACTGAACAGAGAGTAAATAACCTGTATAGACAATTGCTTCTCT

64848 GAGAAATAGCTAATGTAAATGATGAGTTAATGGGTGCAGCAAACCAACATGGCGCATGTA
TACCTGTGTAACAAACCTGCAGGTTGTGCACCTGTACCCTAGAACTTAAAGTACAATAAT
GAAAAAATTAATTAATAAATCAGAAAAAAGAAAGAAAACTGAGGGTTGCCATGG
ATGGTCAAAGTATCTTACATGAGGTCTCAGCAAACTGAAGCAGCAGAGTCTGTATTGAA
ACCCTAAGTCAGCTAACCCCAACCCACGTGCCACAAGAACCCCACTCAAGTTAGAAAAG
[G, -]
TATTAATTAATTTGGAGGCCAAAAACACAGCACATAGACCTCTCAGAAGGGAAAAATAGAA
AATGGGAAAGGATGGAAATGGATTTTCATTTTGTTGATTGAAATTGGGAGATGACTGAATG
AGGAAATATTTTGAATTTTGTGGCCAGGGAAGAGCTGTAAATAGGCAGCAGAAAAGTGGT
TTGAAGAGAAACATACTAAACAAATGCCAGATATTCTTATCTTTACTGGTTATTTTGAAC
TTAGGCAAAATCATACTGAACAGAGAGTAAATAACCTGTATAGACAATTGCTTCTCTTAG

64914 TGTAACAAACCTGCAGGTTGTGCACCTGTACCTAGAACTTAAAGTACAATAATGAAAA
AATTAATTAATAAATCAGAAAAAAGAAAGAAAACTGAGGGTTGCCATGGATGGTC
AAAGTATCTTACATGAGGTCTCAGCAAACTGAAGCAGCAGAGTCTGTATTGAAACCCTA
AGTCAGCTAACCCCAACCCACGTGCCACAAGAACCCCACTCAAGTTAGAAAAGATATTA
AAATATTGGAGGCCAAAAACACAGCACATAGACCTCTCAGAAGGGAAAAATAGAAAATGG
[G, T]
AAAGGATGGAAATGGATTTTCATTTTGTTGATTGAAATTGGGAGATGACTGAATGAGGAAA
TATTTTGAATTTTGTGGCCAGGGAAGAGCTGTAAATAGGCAGCAGAAAAGTGGTTTGAAG
AGAAACATACTAAACAAATGCCAGATATTCTTATCTTTACTGGTTATTTTGAACCTTAGGC
AAAATCATACTGAACAGAGAGTAAATAACCTGTATAGACAATTGCTTCTCTTAGTGCCCA
CCTGGGACTATAAATGCCAGCAGAGAGGTCCACATTTGATTGCGCCTGACCTTGAAAAC

67367 AGGAGGATGTGAGTCAAATTCATTAGGGCCACCCCTAATGCTTTTCACTTAACTAATTA
CATCTACAATGACCCTATTTCCATATAAGATCATATTCTAAAGTAATTGGGGTTAGGACT
TCAACATGTGAATTTTGGGAGCACATAATTCAACCCATAATAGTGACCTTTTACCCAAATC
ATAAAAATTCATCAGGAGATGAGGCTTTAAAAATCACATTAGCCTACCTGATACTTGAAT
CATTTTTTTAAACCAAGCCAAGAAGAGCATTTAGAATTTTAAACAGTATATTTGGCAACAG
[G, A]
GTTTTCGGGTGGATTTTATTTTTTAAACGCCCTCTGTATGCTTCCCAGAATGGTTCCCACT
GCCTACGCCTCGAAGCCTTCATGTTGTCTGGAACAGGTGAGTACTACCTCAGGAAGGGAT
CTTTAAGGGTTCTTTAAGCAGGATTGGAGAGACATTTCCCTGGATCTCAGTCCACTGAAC
AGCAGCCCCCGAGCACTTCCATGTGGGGGCTCTAAGCTGTAGGAAGATGCCTCTGCAAGC
GCCAGACCCCTGAGAGTCTGTAAATTTTTTCTATGAACCATTTTACTTTCACTGAGTTT

67497 AATTTTGGGAGCACATAATTCAACCCATAATAGTGACCTTTTACCATAATCATAAAAAATTC
ATCAGGAGATGAGGCTTTAAAAATCACATTAGCCTACCTGATACTTGAATCATTTTTTTTA
AACCAAGCCAAGAAGAGCATTTAGAATTTTAAACAGTATATTTGGCAACAGGGTTTTTCGGG
TGGATTTTATTTTTTAAACGCCCTCTGTATGCTTCCCAGAATGGTTCCCACTGCCTACGCC
TCGAAGCCTTCATGTTGTCTGGAACAGGTGAGTACTACCTCAGGAAGGGATCTTTAAGGG
[T, A]
TCTTTAAGCAGGATTGGAGAGACATTTCCCTGGATCTCAGTCCACTGAACAGCAGCCCCC
GAGCACTTCCATGTGGGGGCTCTAAGCTGTAGGAAGATGCCTCTGCAAGCGCCAGACCCC
TGAGAGTCTGTAAATTTTTTCTATGAACCATTTTACTTTCACTGAGTTTGGTCTGTTAAA
ATTGTTTTGTGTCCCTCAGCCATGCCCCAGGCCCTGAGAACGAGGGAGTGTTGGTCTGCA
AGAAAACCTAGTGGGTTTATTATTCTCTGACACAGAGAAACCAAATAACATCATTGAGTG

68252 GGGAAATAGTTAGCTAACTAAGCTGTGCCAGGCAACCTCCGGGGCTAAGAAGAACTCAGTGT
TTTCGGACAATGACCAATTACAATAACCAAGTATTATTTGATCTGAGAGTAATTAGCCGAG
GCTCTGTTCTTTTTGCTTCAGTGAGGAGGCAAAAAGGGCAATGAGGAAAACATCAGAGAC

FIGURE 3CC

AGGGGAAACGAGCTCAAATGTCAGAGAAAAACACAGTCTTGACAGGTGGGGAGAAAGTGGAA
GAGTTTCACTGGCCAAGATCCTGACTGAACACTCGAACATTGTTTTCCCTGAAAAATAG
[G, -]
TAGAATTTAACTTAACCAAAAGTTGTTTGAATTCCTTCACTCTTACTGTTCAATTCCTTTA
AAAAGCCTCCACGTAGAATAAAATATCAGGGTACAAAGAGTAAAATAGGTTAGGAACATA
GAACTATGGACTACCAGAGATCTTTCAGTGGGAGGGACAGGTATCTCCAGGACATCTGCA
CCCTCCACTCTTATTTTCAACAGCACTGTATAACCTGAAACCTTTTGGAGACAGGTTCTA
GGGAAGTACTGTTTATCACTTCATTCAAGACGTGCAGTATAGTCAGGCTCCTTCCCCTCT

68580 TGAATTCCTCACTCTTACTGTTCAATTCCTTTAAAAAGCCTCCACGTAGAATAAAATATC
AGGGTACAAAGAGTAAAATAGGTTAGGAACATAGAACTATGGACTACCAGAGATCTTTC
CTGGGAGGGACAGGTATCTCCAGGACATCTGCACCCTCCACTCTTATTTTCAACAGCACT
GTATAACCTGAAACCTTTTGGAGACAGGTTCTAGGGAAGTACTGTTTATCACTTCATTCA
AGACGTGCAGTATAGTCAGGCTCCTTCCCCTCTACCTAGAGATATGTGGATTTTAGCATG
[C, G]
CCCCTGGCTTTCTTTCATGTCACTATCAGCTTCCAAAGTAAATGGCAACTCTCAACCTGA
GAACCATCTTAATACTCCATGCTGCTGCTGCTGCAGCTGCCCCTGTCCCATGGCAGAAGA
TAGTTCACCAGCCTCCTGCTATCACCCACAGCCTTTCTTTCGAGGGCTGAGCAAGGCT
TGAATTCCTGAATACCTCTCTGGCTTTTCTGACGATATAGCACCCATGGCCTCTGCGCC
TTCCTTGTCCCCTAGCAATATGTATTCACCTTTTCTCAGACTTCTGGCTTCTCTGCTCA

69990 CTGTGGATTTGGCTGTTGAATCAGGTTGCAGATGTGGCGAGTAACAAGCAGCCGAAGTGT
CACTGGCTTTTCTACACAATCCCTTCAGAGGTGCAGTGGAACCATTCACAGGCCTGTAGA
TGAATCCCCGGGGCTTGCTTGAGGTTTGATGGTGATCTCCTTAATGTGGGCCTAGTAGGT
ACGCACTCACTTTTATGATTGATTGGCAAAATTGTAGGACAGCTTCTGCAATGTTTCTTCC
TAGTATTGGATGTATTTCTGACTGTGGGCATCTACTACATCCCAAAGTGAAGCAATTTAA
[G, A]
AAGTGCCTACTCTATCCCTGCCCTGTTTCTTCTTCTGTAGGTCTAGGGGGAAAAACCAAAG
AACCAGTTGAGCTCATACTGACCAGCCTGTCTGCACCTCAGAGGTGAGTGGCAGTGCT
GTGGGTGGGAGACTTTTATACTCAGAGCCAGGCTGTGCTAGGAAATCAAAGTCTGTGCC
CAGACCCCTGAGAACAACAGATTTTATGATGATGGAGTGATGGGTTAGTAGATGGTGT
TTACGCAGTCACAAAAGTCAATTTTCAATTTTCTTATTGTTTGTGTTTCTATTCTGGAC

71472 TAGTTAACATCACAAACCTAAGAGTATGAATTCACATTTACCTTGGAAGGTGCTGGTAG
GCAAATTAACATTTGTGATGTTCAATTTTTTATGCCAATGTTTATTTTAAAGTAGGGGT
TGTAACCAAGTGGATAATTGTTCCAGCGGGAGTTAGAGGTGGTGGCCACATGTACAACTAT
GACAGTAAAGGCAATTGGTAACAAGCAAGGCCATAGGTGACAGGAAAAAGCATAATGATA
CAAACACGGAAGATGTGAGTAAATCAACATTTGTGCCCAAAAAGTAACATTTGTTTTCCC
[A, G]
GGACTCTTTCCTCAGCCTTGCAAAAAGAGCTCAATGTGCGATAGCAAGGCGGCGATTACT
GGGGCACTTGCCAAAGGCCAGATCCTAATGGTCTTGCTACCAAGTGCTGCCAGTGAAGGT
TTGTGTTTATGTGGGGTGGAGTTGGCTTGACAGGGGAGACCGACACACTTGGCTCCT
AGGAGGAAGAGACTTCACTTGCCCACTTTGCCCTGGTGACCACCTCTACCGGCGAAGGAG
AAGGAGAAGCAAAGTGCAGCAGTCATAGTTCAGAGGCTGTGAGACTGGAACAAGTCCAGA

71664 AATTGGTAACAAGCAAGGCCATAGGTGACAGGAAAAAGCATAATGATACAAACACGGAAG
ATGTCAGTAAATCAACATTTGTGCCCAAAAAGTAACATTTGTTTTCCAGGACTCTTTCC
TCAGCCTTGCAAAAAGAGCTCAATGTGCGATAGCAAGGCGGCGATTACTGGGGCACTTGC
CAAAGGCCAGATCCTAATGGTCTTGCTACCAAGTGCTGCCAGTGAAGGTTTGTGTTTATG
TGGGGTGGAGTTGGCTTGACAGGGGAGACCGACACACTTGGCTCCTAGGAGGAAGAG
[T, A]
CTTCACTTGCCCACTTTGCCCTGGTGACCACCTCTACCGGCGAAGGAGAAGGAGAAGCAA
AGTGACAGCAGTCATAGTTCAGAGGCTGTGAGACTGGAACAAGTCCAGAAACCACAGAAG
CCCTGAAACAACCTGTGGGGAGGGTGAGGGTAGGTTCTGTTGGTTGAAATGGAATCC
TAAAAAAGAGGTCTTGCACTAATTAGTACCTACCTTCTTTTATTCATTACCTGGTTT
AAAAAAAACAAAAACAAAAACCTGTTCTTATTTTATTTTTTGGAGACAGGCTCTAGTTCT

71677 CAAGGCCATAGGTGACAGGAAAAAGCATAATGATACAAACACGGAAGATGTCAGTAAATC
AACATTTGTGCCCAAAAAGTAACATTTGTTTTCCAGGACTCTTTCCTCAGCCTTGCAAA
AAGAGCTCAATGTGCGATAGCAAGGCGGCGATTACTGGGGCACTTGCCAAAGGCCAGAT
CCTAATGGTCTTGCTACCAAGTGCTGCCAGTGAAGGTTTGTGTTTATGTGGGGTGGAGTTG

FIGURE 3DD

GCTTGTACAGGGGAGACCGACACACACTTGGCTCCTAGGAGGAAGAGACTTCACTTGCCC
[A, G]
CTTTGCCCTGGTGACCACCTCTACCGGCGAAGGAGAAGGAGAAGCAAAGTGCGAGCAGTCA
TAGTTTCAGAGGCTGTGAGACTGGAACAAGTCCAGAAACCACCAGAAGCCCTGAAACAACC
CTGTGGGGAGGGTGAGGGTAGGTTCTGTTGGTTGAAATGGAAATCCTAAAAAAGAGGTC
CTTGCACTAATTAGTACCTACCCTTCTTTTATTCACTTACCTGGTTTAAAAAAAACAAAA
ACAAAAACCTGTTCTTATTTTATTTTGTGAGACAGGGTCTAGTTCTGTCAACCAGGCTA

72590 TCTTGGCTTCCCCAGACACTCTACACAAACACAGTCTAAATAAAAAACAATATGCCTGCCA
TGCTAACACAAGTTTAAACAGGTCTCCAGCCCTTCCCTGTCCAATCAGACTGCAGCCCC
TCAGCCCTCACTACAGGGCAGTTTCAGGAGCCATCTGTTGTGGGTTAATGCTGGGGGAGTA
TTCGAGAGAACAAATCGCTGATTGGGGTGGGACTGTGGAGGTGGAAGTTGATAGATGCAT
TGCTCCCCACCACCTACCCGCCCTCCCATGTCCAGAAGTTCATATTTAACCAGAAAGCA
[T, C]
GAAGCCTGCAGAAAGTGGATTGAGGGCCAAATTTTGGCACAAACTTCACCTCACTACCCA
ATAGTGTGGGTGGACCAGCTAAAATTTGTTTCATGAGATTTCCCTGAGTCTCCTTCCAGA
GAGATCCTAGGCTCTAGTGATTTGTAATAACATTCTCTTCCAAACGTCCATTTTCATGGG
CCCTAAAAAACCTCTGCCTGGACAGGATACCTGGATGAGGAATATATCTGCCAGTCCTT
CTTCAGGCCACAGCAAATGAGTAGACTTCTACACAATTCTTTTTCTCCTAACTGGCCTG

72757 TGCTGGGGGAGTATTTCGAGAGAACAAATCGCTGATTGGGGTGGGACTGTGGAGGTGGAAG
TTGATAGATGCATTGCTCCCCACCACCTACCCGCCCTCCCATGTCCAGAAGTTCATATT
TAACCAGAAAGCATGAAGCCTGCAGAAAGTGGATTGAGGGCCAAATTTTGGCACAAACTT
CACCTCACTACCCAATAGTGTGGGTGGACCAGCTAAAATTTGTTTCATGAGATTTCCCTG
AGTCTCCTTCCAGAGAGATCCTAGGCTCTAGTGATTTGTAATAACATTCTCTTCCAAAC
[G, C]
TCCATTTTCATGGGCCCTAAAAAACCTCTGCCTGGACAGGATACCTGGATGAGGAATATA
TCTGCCAGTCCTTCTTCAGGCCACAGCAAATGAGTAGACTTCTACACAATTCCTTTTTCT
CCTAACTGGCCTGGAAATTTGCAAGGATTTGGAAATTTGCAAATTTCTTCTCTATCTTGC
CTATGAAGCAATTATTCTGAGTTTGAAAGTAGTTATCTGTTTGCAAAACAGTTTCATG
TCTTGGGAATCAAATAGCTCAAATTTTAAATGCAAATCTTATGCAAAAAATTAGGTAAAT

72863 CAGAAGTTCATATTTAACCAGAAAGCATGAAGCCTGCAGAAAGTGGATTGAGGGCCAAAT
TTTGGCACAAACTTCACCTCACTACCCAATAGTGTGGGTGGACCAGCTAAAATTTGTTCA
TGAGATTTCCCTGAGTCTCCTTCCAGAGAGATCCTAGGCTCTAGTGATTTGTAATAACA
TTCTCTTCCAAACGTCCATTTTCATGGGCCCTAAAAAACCTCTGCCTGGACAGGATACCC
TGGATGAGGAATATATCTGCCAGTCCTTCTTCAGGCCACAGCAAATGAGTAGACTTCTAC
[A, C]
CAATTCTTTTTCTCCTAACTGGCCTGGAAATTTGCAAGGATTTGGAAATTTGCAAATTT
CTTCTCTATCTTGCCTATGAAGCAATTATTCTGAGTTTGAAAGTAGTTATCTGTTTGCA
GAAACAGTTTCATGTCTTGGGAATCAAATAGCTCAAATTTTAAATGCAAATCTTATGCA
AAAATTAGGTAATTAAGAATTCTGGGCCAAGACTTCCAGCATCTCTGCATCATGGCACCT
GGAAGGGAAATAATATCTGATCTTTCTTGCTTAAAGTCAGTAGGTGTATTTGACATTAAG

74565 AAGATCAACTTGAGGATTTGTCTTACTGTGATTTAAGTACTTAATTCTCTCTCTTCTCCTC
TGCTCCATCTCAAGGGAACCAAGAGAGCTTCTAACTAATAAGACTGGGTGAGCTTCAGA
AATGCTGCAACAAGTGATTTTCTACCCAAGCTTCACCCCTCCAGAATCACCTCTTTAGA
ATTCTGTGCTTTTCCCTCCAGATTTCTGTGCTTGCCACCCTTGAGTCCAGAGCCTTG
AACATGTTTTTGTGTTGTTGTTGAGACAGAGTCTGTTCTGTTGCCAGGCTGGAGTG
[C, T]
TGTGGTGCAATATTAGCTCACTGCAGCCTCTACCTCCAGGTGCAAGTGATTGTATGCC
TCAGCCTCCTGAGTAGCTGGGATTACAGGTGCATGCCACCACGCCAGCTAATTTTTATG
TTTTTAGTAGAGACAGGGTTTCGCCATGTTGGCCAGTCTGGTCCCAAACCTCTGGCCTCA
AGTGATCTGCCTACCTCAGCCTCTCAGAGTTCGATCGTATTTTGAATCAGGCCTTTCTAC
TTGGTTGGGGCTGCAGTGTTCTCCAAAAAGAATCCTTGATTATATATTTCTGTTTATAA

74850 GCCCAGGCTGGAGTGCTGTGGTGCAATATTAGCTCACTGCAGCCTCTACCTCCAGGTGC
AAGTGATTGTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCATGCCACCACGC
CCAGCTAATTTTTATGTTTTTAGTAGAGACAGGGTTTCGCCATGTTGGCCAGTCTGGTCC
CAAACCTCTGGCCTCAAGTGATCTGCCTACCTCAGCCTCTCAGAGTTCGATCGTATTTTG
AATCAGGCCTTTCTACTTGGTTGGGGCTGCAGTGTTCTCCAAAAAGAATCCTTGATTAT

FIGURE 3EE

[A, G]
TATTTCTGTTTATAATTATATTTCTGTGCTTTTTATGTGTACATGGTGCCCAGACACACG
GTGGAGGGCAAGGGAGCTGAGTGATAGAATGAGGAGATTTTTCCCTTCAACTTAGTAAC
AGGACAGTCAGTAAGAGTTTTAGTATGGGGGTTACTTTTCCAGTTGCCATCAACTTTAGCA
ATTCAGGAAAATTCTACTTAAATCTAAGTCTAGCCATCTCCTTTTCTTTACTTTTTGT
TTTTATCCCTTTGTTTTTGAAGGGAGGCTGCTGGAGAACTCTATTTTTCTCTCCAC

75462 GGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCAGATGCTAAAAGGCTTTCCAGAGA
CCGCGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTAGCGCCCTGCCATCTCAGCT
GTACCAGCTTCTGATGGTGAGCGAGGGAGTGTGTGCGTGTGCGTGAGTGTCATGTGCGTG
AGTGCGTGTGTGTGTAAGTCTTGGTGTCTTAAGTAGTTTGCCTCAGCACCGGAGAATCAT
AGCATTTACCCCCAGGAGTGAAGTTAGAGATCAGTTTGCCTGGGAGAAGCAAGATAGGAC
[G, C]
TAATCTTGTCTGAGTTTTGCATGAGCTTCTCTCAAACTCTGAAGCACTGGTGGGGAGAGG
TTACAAGACCTCTTTGTAATGGTCCAGACATTTACAGGTACACATTTACACTCAGAAA
TTGGATGAGATGGACGTTGTCTCTGAGTTGTTTTGCCTTAGCTACCATCTGCCAGGAAGCC
ACACCAGTGTCTTAACAAGACTCTTCTCCCTTTCTGCGGAGAGTAAGATGATAGGTGAA
GCGGATATGTCCTGAGAGGGAGCTGGGCCTTTCTTGATTGGTAATAGCAAGCTGCAGAAG

76045 AATAGCAAGCTGCAGAAGGCAGTGCCGGGGTGGGGTGCTGGGGGAAGGGAGGTCTCCTCC
GAGGCTGCCACCTCCTGTAAACACAAGTTACCTTGAATCAGCCTTTGCTGCCTGGGCC
TGAAGTCATCTTCCAAACCTGAAATCTGCTGAGGGATCATGTGGTTGGAATCCCGTCAT
GTTTCTTGGACTGTGGCCAGGAAGGGCTACAGGAGGATGTGGGCAGTGGTCATGGGGGAC
TATCCTTAGGTGAGGTTCTTTGAAAAAATCCACCATTCAACTAAAAATAGTTTTAGGA
[A, G]
CAAGGGACAAGTAGACAAGAAAAGCAAAGCTACCAGGAAGGAAAAACAGAAGAGAGAGAA
GCAGCCAGGGTTGGTTTTAGAAGTCTAAGCCAGAGAAAAGAAAGCTTAGGAGGGAGGGC
CTAAGGGCTGGAAGTGCATGAGGACACTGGAAGGGGCGTGGGGGAGTGCGCATGGGGTG
CAGTGAGATAAGGATGGGGACAGGGTGAGGAGCTACTGCCCAAGAGGTGTGGAAACAGCC
TGGTCCGCCTTGCCAGAGTTTGCAGACGCAGCTCCTCTGTGTCTAGGACATCGTCTGCA

79973 ACTTCAGGCCTTCTTTGAGTGTTATCTCCTTAATATATTGGAAGGTCCCTATGATATCAC
TTCCCAAAGGCCACTTTAGGCTGAATTCCTTTAACCTTTGTTTCCAAATACAAATTCGT
TTCTCCCACTTTTTAGTCATT!TGTTTTATTGTTCTTCTGAATCTGTTCCAATTTATTT
TGCTTATCTCTGAGAATATGGAGGCAGCATAGACTCAAATTTCTTGCATGGTGGGAGAAT
CATGTTCCATTATTGAGGTTTACTGAGTGTCCATGAGGTGTGATATTAAGGAT
[G, A]
CAAAAATGAATTAGTCATAGACCTGTCTCTCAAAGAGCTTACGGTCTTTAGGAAAATAAG
ACAAGTATATAAACAGCTGCAGATCAAGTATACAAATAAAGTGCTCTAAGTGTGTTGAAGG
AGGTGAGATTAACTCCAGCTGTGGGGATCCAGGATGATTTTGTGAGTGGGCCTTGAAAGA
TGATGGGTCTGGATGATTGGAGAGGAAGGGCATACGGGCAAAGGAATGTCGTGTTCTCT
CAATACCATCTAAGATCATTCTGAAGTTGTCTTTTAAATCATAGTGGCTCAGTCTTA

83181 ATGTATGTGATTGTGCCCCTAGTCAGAGTTTTAAGTGCACTTCGTGTTAGTTAGCAACT
TCAATTTAAAGTGCTGTGTGATCCTCTGGGCTTTGAAGATATGAATTCCTATACATACA
CATGAGCTAAAATTACCGCATAATCACGAGGATGTGTGCACTTTGAATAATTGAATGCAC
TAAACATCTCCAGCTGATGGATTGATGATGTGGGAGAGTAGTGCAAAACCCACGTGACAC
GGAAGATTACAAGACATTTTGAATGATAGCTTAATTTTCAACCTTTTTTTTTTTTTTTT
[-, T]
GCTTGTGCTTTCTTTTTAGCGATTATGGGCAAGTAAAAGAGATTTGATTATCTTGTTTT
CTGTGAAAGGTTATTTAGCCCTCAATCCCATTAAAGTCACTTTCTGCACTCCAGTGCACT
GAGCCTTCAGGTTATCAGCCAGGAAGAGTAAATGGAGACACCAGGATCAGATTTCTAAA
GGAAGGAAAGTTAAAGCAAAGTTTGAAGGGGTGACAGCCAACAGCCATGAGCTTAGGAA
CTCAATTAGACTAAAAGACAACATATCTCATTATCTCGTTCGAAATGATCTAAATACAT

84935 GAAGTTTTATTTCCGTACTTTTTCAGATAAGCCCCTTGCAATGTCAACTTTTGGAGGAAC
TGGCTTGTAGCTTTAGTGTAGTGAGCATTAGGAGTAGCAAGCACTTAACAAACACAGGC
ACTTGGGAAAATGCGAACTGCCAGTATTCTGAGCTAACCAATACCTGATTTGGACATCA
AAGGTAGTATATATATTTTCAAATAGTTTTTTTTTTCTCAATTTGCAAAAGTTGCACCTT
AGAGTCTATATAAATAGATTGCCAGCCAGGCCCCGAGGCTCATGCCTATGATCCCAGCAC
[C, T]

FIGURE 3FF

TTGGGAGGCTGAGGCAGGTGGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAAC
GTGGTGAAACCTTGTCTCCATTAATAAATACAAAAATTAGCCAGATGTGGTGATGCTTGCC
TGAGTCCCAGCTACTGCGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAAGTGGAGG
CTGCAGTGAGCCGAGATCACCCCACTGCACTCCAGCCTGGGCCACAGAGTGAGACTCAGT
CTCAAAAAAGAAAAAAAAAAAAAAAAAAGATTGCCTAATGTATCTAACAAAAATTGGAAA

87476 AGATATCGGCTTCCTGGCTCTTCTAAGATCATTGTCTTGTCTTCAAAGAGCAGGGAAGTT
TAAAATTATAGCTGATCCTCAGAGCATTTTATGAAATACCTAAGTTTGATTTTGACAAT
ATACATTTAGAATTACAATTGGTGATATAATATGGTATTTCCCAAGCAAAATATTCTCTA
GAGCAGAGCTTTTACTGTATAATTATTTTAAACCTGCTAGTTATAAGGACAGAATGAACT
TTAGCTGCATTCTGTGAAGTGGAGGGCCTTACCCTTCATAAAATTATCAAAGATACTAAT
[C,G]
GAAATGGGCTCAGATGGTGGTGCTCCATTAACATTATTATTATTTCTATTGTTGTTATTT
TATTTTCTTAAGCAGCTGGAAGGTAGGGAGATAACCTTGCCTTTCTGATCTACAGTGACC
TTCCACAAAAAATTGCTACCTGTAGACATAAATTGGTCACAATAGAAAAATCAATTAAATG
CAGCATGTCAAGCTTGTGGCCTGCGCCAGCAATTGAAGAAGGGAGAAAGGCAGATTTTGCC
TCTGCTGGAGTAAGCTCATGATGTCCCTAGGCCTTGGTACGAATGTAAGGAGATAAACT

FIGURE 3GG